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Sequence 765, Apple Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 2, Appl Sequence 2, Appl Sequence 62, Appl Sequence 61, Appl Sequence 61, Appl Sequence 61, Appl Sequence 61, Appl
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                                                                                June 7, 2005, 14:31:10 ; Search time 43 Seconds (without alignments) 253.460 Million cell updates/sec
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1. /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2. /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3. /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

4. /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5. /cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*

5. /cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*

6. /cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-513-999C-7655
US-09-130-663-29
US-09-432-335-29
US-09-644-022-29
US-08-467-603-2
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US-08-467-603-6
US-08-467-603-62
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US-09-374-671A-63
US-09-690-454-221
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US-08-466-793-63
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Maximum Match 1008
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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US-09-800-729-202
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US-08-825-891-1
US-08-825-891-1
US-09-949-016-9658
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US-09-332-934-14
US-09-332-934-14
US-09-312-934-14
US-09-919-497-88
US-09-949-016-10788
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Sequence 2, Application US/09130663A
Patent No. 6020163
GENERAL INFORMATION:
APPLICANT: CONKlin, Darrell C.
TITLE REFERENCE: 97-24
CURRENT APPLICATION NUMBER: US/09/130, 663A
CURRENT PILING DATE: 1998-08-05
EARLIER RPPLICATION NUMBER: 60/054,867
CURRENT PILING DATE: 1997-08-06
SEQ ID NO. SEQ ID NOS: 30
SEQ ID NO. SEQ ID NOS: 30
LENGTH: 170
TYPE: PAT.
CORGANISM: HOMO Sapiens
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US-09-432-335-2
US-09-432-335-2
; Sequence 2, Application US/09432335
; Patent No. (143720)
; GENERAL INFORMATION:
    TILE REPERENCE: 97-24
CURRENT APPLICATION NUMBER: US/09/432,335
; CURRENT FILING DATE: 1999-11-02
; EARLIER FILING DATE: 1999-11-02
; EARLIER FILING DATE: 1998-08-06
; EARLIER FILING DATE: 1998-08-06
; EARLIER FILING DATE: 1998-08-06
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APPLICATION NUMBER: US/09/690,454

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                                                                                                                                                              Length 170;
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Pred. No. 6.8e-69;
4; Mismatches 7; Indels
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| Patent NO. 6365716
| GENERAL INFORMATION: APPLICANT: CONKIN, Darrell C. TITLE OF INVENTION: LIPOCALIN HOMOLOG FILE OF INVENTION: LIPOCALIN HOMOLOG CURRENT APPLICATION NUMBER: US/09/614,022 CURRENT FILING DATE: 2000-07-11
| PRIOR APPLICATION NUMBER: 09/130,663 |
| PRIOR FILING DATE: 1998-06 |
| PRIOR FILING DATE: 1997-08-06 |
| NUMBER OF SEQ ID NOS: 30 |
| SOFTWARE: FastSEQ for Windows Version 3.0 |
| SEQ ID NO 2: SEQ ID NOS: 30 |
             NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
EARLIER FILING DATE: 1997-08-06
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Best Local Similarity 91.5%;
Matches 119; Conservative
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ORGANISM: Homo sapiens
                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
                                                                     LENGTH: 170
                                                                                                                             US-09-432-335-2
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US-09-614-022-2
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NAME/KEY: SITE LOCATION: (21)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-690-454-78
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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Fatent No. 67839961
GENERAL INCORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, APPLICANT: Glordano, J.Y.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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CURRENT APPLICATION NUMBER: US/09/690,4
PRIOR FILING DATE: 2000-10-18
PRIOR APPLICATION NUMBER: 09/189,144
PRIOR APPLICATION NUMBER: 60/044,039
PRIOR APPLICATION NUMBER: 60/044,039
PRIOR FILING DATE: MAY 30, 1997
PRIOR PILING DATE: MAY 30, 1997
PRIOR FILING DATE: MAY 30, 1997
PRIOR FILING DATE: AUGUST 29, 1997
PRIOR PILING DATE: AUGUST 29, 1997
PRIOR FILING DATE: AUGUST 29, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (18)
OTHER INFORMATION: Xaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            141 GH 142
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59

Sequence 78, Application US/09690454
Patent No. 6531447
GENERAL INFORMATION:
APPLICANT: Steven M. Ruben, et al.
TITLE OF INVENTION: 32 Human Secreted Proteins
FILE REFERENCE: PZ006P1

RESULT 4 US-09-690-454-78

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MKTLFLGVTLGLAAALS----FTLEEE--DITGTWYVKAMVVDKDFPEDRRPRKVSPVKV 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34 MVVDKDFPEDRRPRKVSPVKVTALGGGNLEATFTFMREDRCIQKKILMRKTEEPGKFSAY
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35.1%; Score 274.5; DB 3; Length 176;
Best Local Similarity 42.3%; Pred. No. 8.8e-26;
Matches 58; Conservative 27; Mismatches 41; Indels 11
                                                                                                                                                                                                                                                                                                                              Length 66;
                                                                                                                                                                                                                                                                                                                                                                2; Indels
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41.0%; Score 321; DB 4;
Best Local Similarity 93.9%; Pred. No. 4.2e-32;
Matches 62; Conservative 2; Mismatches 2
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GENERAL INFORMATION:
APPLICANT: CONKLIN, Darrell C.
TITLE OF INVENTION: LIPOCALIN HOMOLOG
FILE REFERENCE: 97-24
CURRENT APPLICATION NUMBER: US/09/130, 663A
CURRENT FILING DATE: 1998-08-05
BARLIER PILING DATE: 1997-08-06
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 3:0
ELENGTH: 176
Patent No. 6783961
PILE REFERENCE: 59.US2.REG
CURRENT PEDFLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SOFTWARE: Patent.pm
LENGTH: 66
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                                                                                                                                                                                                                                                                       CTHER INFORMATION: Xaa=His or Pro
US-09-513-999C-7655
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                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
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Sequence 29, Application US/09432335 Patent No. 6143720 GENERAL INFORMATION:

US-09-432-335-29

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55 TALGGGNLEATFTFWREDRCIQKKILMRKTEEPGKFSAYGGRKLIYLQELPGTDDYVFYC 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MKTLFLGVTLGLAAALS----FTLEEE--DITGTWYVKAMVVDKDFPEDRRPRKVSPVKV 54
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                                                                                                                                                                                                                                                                                                                                                                                             Length 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                          41; Indels
                                                                                                                                                                                                                                                                                                                                                                                               DB 3;
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35.1%; Score 274.5; DB 3
Best Local Similarity 42.3%; Pred. No. 8.8e-26;
Matches 58; Conservative 27; Mismatches 41
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; Sequence 29, Application US/09614022
; Sequence 29, Application US/09614022
; Patent No. 6365716
; GENERAL INFORMATION:
; APPLICANT: CORALIN, Darrell C.
TITLE OF INVENTION: LIPOCALIN HOMOLOG
; FILE REFERENCE: 97-24
; CURRENT PELLING: DATE: 2000-07-11
; PRIOR FILLING DATE: 1998-08-06
; PRIOR FILLING DATE: 1997-08-06
; PRIOR FILLING DATE: 1997-08-06
; PRIOR FILLING DATE: 1997-08-06
; NUMBER OF SEQ ID NOS: 30
; SEQ ID NOS: 30
; SEQ ID NO 2: 30
; SEQ ID NO 2: 30
APPLICANT: Conklin, Darrell C.
TITLE OF INVENTION: LIPOCALIN HOMOLOG
FILE REFERENCE: 97-24
CURRENT APPLICATION NUMBER: US/09/432,335
CURRENT FILING DATE: 1999-11-02
BARLIER FILING DATE: 1999-11-02
BARLIER FILING DATE: 1999-10-08-06
BARLIER FILING DATE: 1997-08-06
SARLIER FILING DATE: 1997-08-06
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 29
LENGTH: 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           115 KDQRRG----GLRYMGK 127
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US-09-432-335-29
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Best Local Similarity
Matches 58; Conserv
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USA
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CITY: Boston
                                                                                                                                                                          STATE: MA
COUNTRY: US
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US-08-491-861A-2
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Best Local Similarity 35.7%; Pred. No. 5.1e-22;
Matches 50; Conservative 29; Mismatches 45; Indels 16; Gaps
                                                                    APPLICANT: Morgenstern, Jay P.
APPLICANT: Kanieczny, Andrzey
APPLICANT: Bizindaukas, Christine B.
APPLICANT: Brauer, Andrew W.
TITLE OF INVENTION: Allergenic Proteins and
TITLE OF INVENTION: Peptides from Dog
TITLE OF INVENTION: Peptides from Dog
TITLE OF INVENTION: Dander and Uses Therefor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
APPLICATION NUMBER: 07/999,712
FILING DATE: 31-Dec-92
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-026CP (IPC-048CP)
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/156,549
                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: ASCII-text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,603
                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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115 ILYCEGELHGRQIRMAKLLG 134
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Patent No. 5891716
GENERAL INFORMATION:
APPLICANT: Morgenstern, Jay P.
APPLICANT: Kanieczny, Andrzey
US-08-467-603-2; Sequence 2, Application US/08467603; Patent No. 5843672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                02109
                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-467-603-2
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51 PVKVTALGGGNLEATFTFMREDRCIQKKILMRKTEEPGKFSAYGGRKLIYLQELPGTDDY 110
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35.7%; Pred. No. 5.1e-22;
tive 29; Mismatches 45; Indels 16; Gaps
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APPLICANT: Kanieczny, Andrzey
APPLICANT: Kanieczny, Andrzey
APPLICANT: Bizindaukas, Christine B.
APPLICANT: Brauer, Andrew W.
TITLE OF INVENTION: Allergenic Proteins and Peptides from Dog TITLE OF INVENTION: Dander and Uses Therefor CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
PELLICATION NUMBER: US/08/466,793
FILING DATE: 06-JUN-1995
CLASSIFICATION NUMBER: US/08/156,549
FILING APPLICATION NUMBER: US/999,712
FILING DATE: 22-NOV-1993
APPLICATION NUMBER: US/999,712
FILING DATE: 31-Dec-92
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REFERENCE/DOCKET NUMBER: IMI-026CP(IPC-048CP)
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATI
APPLICANT: Bizindaukas, Christine B.
APPLICANT: Brauer, Andrew W.
TITLE OF INVENTION: Allergenic Proteins and
TITLE OF INVENTION: Peptides from Dog
TITLE OF INVENTION: Dander and Uses Therefor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: LAHIVE & COCKFIELD, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 2, Application US/08491861A; Patent No. 5939283; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              111 VFYCKDQRRGGLRYMGKLVG 130
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115 ILYCEGELHGRQIRMAKLLG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     174 amino acids
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Best Local Similarity 35.7*
Matches 50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-08-466-793-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
TOPOLOGY: linear
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51 PVKVTALGGGNLEATFTFMREDRCIQKKILMRKTEEPGKFSAYGGRKLIYLQELPGTDDY 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MKTLFLGVTLGLAAALSFTLEEED------ITGTWYVKAMVVDKDFPEDRRPRKVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45; Indels
        CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/374,671A
FILING DATE: 16-Aug-1999
FRICH APPLICATION DATA:
APPLICATION NUMBER: US 08/156,549
FILING DATE: 1993-NOV-22
APPLICATION NUMBER: US 07/999,712
FILING DATE: 1992-DEC-31
ATTORNEY/AGENT INPORMATION:
NAME: DIGIOGIO, Jeanne M.
REGISTRATION NUMBER: 41,710
REFERENCE/DOCKET NUMBER: IMI-026C2CNCPA
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 742-4214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 62, Application US/08467603
Fatent No. 5843672
GENERAL INFORMATION
APPLICANT: Morgenatern, Jay P.
APPLICANT: Bizindaukas, Christine B.
APPLICANT: Bizindaukas, Christine B.
APPLICANT: Bizindaukas, Christine B.
TITLE OF INVENTION: Allargenic Proteins and TITLE OF INVENTION: Peptides from Dog TITLE OF INVENTION: Dander and Uses Therefor NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 31.2%; Score 244; DB 4; Best Local Similarity 35.7%; Pred. No. 5.1e-22; Matches 50; Conservative 29; Mismatches 45
                                                                                                                                                                                                                                                                       E: LAHIVE & COCKFIELD
60 State Street, suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/156,549
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: ASCII-text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
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US-08-467-603-62
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TITLE OF INVENTION: Allergenic Protein and Peptides from Dog
Dander and Uses Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45; Indels
                                                                                  COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBW PC comparible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII-text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/491,861A

FILING DATE: 3-Cor-1995

CLASSIFICATION DATA:

APPLICATION NUMBER: 07/999,712

FILING DATE: 31-Dos-1

ATTORNEY AGENT INFORMATION:

NAME: Mandragouras, AMY E.

REGISTRATION NUMBER: 36,207

REPERENCE/DOCKEY NUMBER: 1MI-026CP(IPC-048CP)

TELEPHONE: (617) 742-4214

INFORMATION FOR SEQ 1D NO: 2:

INFORMATION FOR SEQ 1D NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
31.2%; Score 244; DB 2;
Best Local Similarity 35.7%; Pred. No. 5.1e-22;
Matches 50; Conservative 29; Mismatches 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZDF: 02100
ZDF: 02100
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Morgenstern, Jay P.
Konieczny, Andrzej
Bizindaukas, Christine B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Amy E. Mandragouras
STREET: 28 State Street
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Patent No. 6489118
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 174 amino acids
amino acid
                    28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , MOLECULE TYPE: protein.US-08-491-861A-2
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STREET: 2C -- TW: Boston
                                                                            USA
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Gaps

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25 ITGTWYVKAMVVDKDFPEDRRPRKVSPVKVTALGGGNLEATFTFMREDRCIQKKILMRKT 84
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INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 144 amino acids TYPE: amino acid
                        LENGTH: 144 amino acids
SEQUENCE CHARACTERISTICS
                                                             TOPOLOGY: Illnear

MOLECULE TYPE: peptide

7: FRAGMENT TYPE: internal

18-08-466-793-62
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                                           amino acid
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ZIP: 02109
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                                                                                                                                                                                                                                                                                                                                                                                                                   29.4%; Score 230; DB 2; Length 144; 38.7%; Pred. No. 2.16-20; Live 26; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85 EEPGKFSAYGGRKLIYLQELPGTDDYVFYCKDQRRGGLRYMGKLVG 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII-text
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/466,793
FILING DATE: 06-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/156,549
FILING DATE: 2-NOV-1993
APPLICATION NUMBER: US/09/93,712
FILING DATE: 31-Dec-92
ATTORNEY/AGENT INFORMATION:
NAME: MAINTERMATION NUMBER: 36,207
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: 36,207
REFERENCE/DOCKET NUMBER: 36,207
TELECOMMUNICATION NUMBER: 36,207
                 FILING DATE: 31-Dec-92
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: 1M1-026CP(IPC-048CP)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 62: SEQUENCE CHARACTERISTICS:
LENGTH: 144 amino acids
TYPE: amino acids
TYPE: amino acids
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Morgenstern, Jay P.
APPLICANT: Kanleczny, Andrzey
APPLICANT: Braineczny, Andrzey
APPLICANT: Brauer, Andrew W.
TITLE OF INVENTION: Allergenic Proteins and
TITLE OF INVENTION: Peptides from Dog
TITLE OF INVENTION: Dander and Uses Therefor
WUMBER OF SEQUENCES: 104
CORRESPENDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 60 State Street, suite 510 CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 62, Application US/08466793
Patent No. 5891716
GENERAL INFORMATION:
APPLICATION NUMBER: 07/999,712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41; Conservative
                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 41; Conserva
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COUNTRY: US.
ZIP: 02109
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                                                                                                                         25 ITGTWYVKAMVVDKDFPEDRRPRKVSPVKVTALGGGNLEATFTFMREDRCIQKKILMRKT
                                                                 Gaps
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                                                                 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Morgenstern, Jay P.
APPLICANT: Kanieczny, Andrzey
APPLICANT: Bizindaukas, Christine B.
APPLICANT: Bizindaukas, Christine B.
TITLE OF INVENTION: Allergenic Proteins and Peptides from Dog TITLE OF INVENTION: Dander and Uses Therefor NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5
Query Match 29.4%; Score 230; DB 2; Length 144; Best Local Similarity 38.7%; Pred. No. 2.16-20; Matches 41; Conservative 26; Mismatches 37; Indels
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                                                                                                                                                                                                                                             85 EEPGKFSAYGGRKLIYLQELPGTDDYVFYCKDQRRGGLRYMGKLVG 130
                                                                                                                                                                                                                                                                               63 SEPGKYTAYEGORVVFIQPSPVRDHYILYCEGELHGRQIRMAKLLG 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-026CP(IPC-048CP)
TELECOMMUICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPAX: (617) 742-4214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII-text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/491,861A
FILING DATE: 27-OCT-1995
CLASSIFICATION: 435
PRIOR APPLICATION UNBER: 07/999,712
FILING DATE: 31-DEC-92
FILING DATE: 31-DEC-92
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-491-861A-62
; Sequence 62, Application US/08491861A
; Patent No. 593928
; GENERAL INFORMATION:
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5 VSGKWYLKAMTADQEVPE--KPDSVTPMILKAQKGGNLEAKITMLTNGQCQNITVVLHKT 62
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Search completed: June 7, 2005, 14:41:04 Job time: 44 secs

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RESULT 1
                                                                                                          June 7, 2005, 14:26:40 ; Search time 160 Seconds (without alignments) 352.919 Million cell updates/sec
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782
1 MKTLFLGVTLGLAAALSFTL......KLVGPCRCPHVGSPGHLTCR 146
                                                                                                                                                                                                                                                                                                                                                               2105692
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                          2105692 segs, 386760381 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                           OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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geneseqp2003bs:*
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Maximum DB seq length: 2000000000
                                                                                                                                                                                           Title:
Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

					SUMMAKIES	
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Result		Query				
No.	Score	Match	Match Length	DB	ID	Description
	782	100.0	146	4	AAB67739	Aab67739 Amino aci
8	687.5	87.9	228	4	AAM78682	Aam78682 Human pro
m	687.5	87.9	228	4	AAB67740	-
4	619	86.8	170	4	AAB67738	Aab67738 Amino aci
·	646.5	82.7	221	4	ABG11868	Novel
9	623	7.67	170	7	AAW99669	Aaw99669 Human lip
7	623	79.7	170	~	AAW95641	Human
80	623	79.7	170	m	AAB33450	Aab33450 Human PRO
6	623	79.7	170	m	AAY99389	Aay99389 Human PRO
10	623	79.7	170	4	AAB66138	Aab66138 Protein o
11	623	79.7	170	4	AAB67742	Aab67742 Amino aci
12	623	79.7	170	S	ABB84919	Human
13	623	79.7	170	'n	AAE22099	Aae22099 Human Zli
14	623	79.7	170	ß	ABB95525	
15	623	79.7	170	9	AB033631	Novel
16	623	79.7	170	7	ABO44484	Abo44484 Human sec
17	623	79.7	170	7	AB033508	Abo33508 Novel hum
18	623	79.7	170	7	ADC18031	Adc18031 Human PRO
19	623	79.7	170	7	ADD10495	Add10495 Human sec
20	623	79.7	170	7	ADD11455	Add11455 Human sec
21	623	79.7	170	~	ADD70677	Add70677 Human sec
22	623	79.7	170	7	ADD39754	Add39754 Human sec
23	623	79.7	170	7	ADD70200	Add70200 Human sec
24	623	79.7	170	2	ADD37248	Add37248 Human sec
25	623	79.7	170	7	ADD38321	Add38321 Human sec

Add39277 Human sec	Add38800 Human sec	Add40231 Human sec	Ade50452 Human sec	Ade20064 Human sec	Ade49975 Human sec	Ade21533 Human sec	Adf29958 Human sec	Adf55851 Human sec	Adh99355 Human sec	Ade41456 Human sec	Ade96535 Human sec	Adf25846 Human sec	Adf24745 Human sec	Adf29481 Human sec	Ade97012 Human sec	Adh03050 Human sec	Adh04004 Human sec	Adh03527 Human sec	Adh43639 Human PRO	
ADD39277	ADD38800	ADD40231	ADE50452	ADE20064	ADE49975	ADE21533	ADF29958	ADF55851	ADH99355	ADE41456	ADE96535	ADF25846	ADF24745	ADF29481	ADE97012	ADH03050	ADH04004	ADH03527	ADH43639	
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170	170	170	170	170	170	170	170	170	170	170	170	170	170	170	170	170	170	170	170	
79.7	79.7	79.7	79.7	79.7	79.7	79.7	79.7	79.7	79.7	79.7	79.7	79.7	79.7	79.7	79.7	79.7	79.7	79.7	79.7	
623	623	623	623	623	623	623	623	623	623	623	623	623	623	623	623	623	623	623	623	
26	27	28	29	30	31	32	33	34	35	36	37	38	36	40	41	42	43	44	45	

ALIGNMENTS

Odorant binding polypeptide; OBP; hydrophobic ligand; odorant; allergy; asthma; cancer; perfume; hyperlipidemia; obesity; food additive; anticancer; foetus detoxification; pregnancy marker. Amino acid sequence of odorant binding polypeptide OBPIIa-beta. ... [14 AAB67739 standard; protein; 146 AA. Gachon 99FR-00010439. 11-AUG-2000; 2000WO-FR002319 (first entry) வ் (UYAU-) UNIV AUVERGNE. (PITI/) PITIOT G. Lacazette WPI; 2001-202864/20. N-PSDB; AAF80040. WO200112806-A2. Homo sapiens. 12-AUG-1999; 22-FEB-2001. 11-JUN-2001 Pitiot G, AAB67739; AAB67739

New human odorant-binding proteins, useful for solubilizing lipophilic compounds in the transportation of anticancer agents or for slow release of perfumes.

Claim 2; Page 109; 132pp; French.

The present sequence represents a human odorant binding polypeptide (OBP), designated OBPIIa-beta. OBPs provide long-term retention (gradual release) of lipophilic compounds, so prolong the 'hold' of perfumes, deodorants etc. . OBP polypeptide are used as binding proteins for hydrophobic ligands (particularly odorants); as competitive inhibitors (agonists or antagonists) of cellular lipocalcin receptors; to detect specific antibodies for diagnosis of alleasy, asthma or cancer; for controlling volatilisation of an odorant, specifically in perfumes, cosmetics or disinfectant compositions; to screen compounds, especially odorants or flavours, e.g. human pheromones, for binding to OBP, also in

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                       for treating hyperlipidemia or obesity, or to supplement non-maternal malk when combined with mutritional fatty acids, as food additives; as a transporter of pharmaceuticals, especially anticancer agents (providing delayed release) but also for delivery across the placental barrier (e.g. for detoxification of the foetus); as a marker of pregnancy or foetoplacental pathology (rupture of the amniotic membrane); and as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy.
complex perfume mixtures; to solubilise lipophilic compounds;
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R, Wang ZW;
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                                                                                                                                                                                                                                                                                                    100.0%; Score 782; DB 4;
100.0%; Pred. No. 9.8e-85;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM78682 standard; protein; 228 AA
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2000US-00598075.
2000US-00620325.
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15-SEP-2000; 2000US-00653561.
20-OCT-2000; 2000US-00693325.
30-NOV-2000; 2000US-00728422.
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Best Local Similarity
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, Yang Y,
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                                                                                                                                                                                                                                                   Sequence 146 AA;
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20-JUN-2000;
19-JUL-2000;
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Matches 146;
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Ma Y, Zh
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The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, immunoomodulatory activities activity, tissue growth factor activity, immunoomodulatory activity and activiny, inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leuksemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52822) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication
                                                                                                                                                                                                                                                                                                                                                                                                                                              NLEATFTFMREDRCIOKKILMRKTEEPGKFSAYGGRKLIYLQELPGTDDYVFYCKDQRRG 120
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Pred. No. 3.4e-73;
1; Mismatches 6; Indels 3:
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                                                                                                                                                                                                                                                                    Sequence 228 AA;
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Claim 2; Page 107; 132pp; French.
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release) of lipophilic compounds, so prolong the 'hold' of perfumes, designated OBPPINA-gamma. OBPB provide long-term retention (gradual release) of lipophilic compounds, so prolong the 'hold' of perfumes, deciderants etc. OBP polypeptides are used as binding proteins for hydrophobic ligands (particularly odorants); as competitive inhibitors (agonists or antagonists) of cellular lipocalcin receptors; to detect specific antibodies for diagnosis of allergy, asthma or cancer; for controlling volatilisation of an odorant, specifically in perfumes, cosmetics or disinfectant compositions; to screen compounds, especially odorants or flavours, e.g. human pheromones, for binding to OBP, also in complex perfume mixtures; to solubilise lipophilic compounds; for treating hyperlipidemia or obesity, or to supplement non-maternal mik when combined with nutritional fatty acids, as food additives; as a transporter of pharmaceuticals, especially anticancer agents (providing delayed release) but also for delivery across the placental barrier (e.g. for decoxification of the foetus), as a marker of pregnancy or foeto-
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                                                                                                                                                                                                                                                                                                  3,
                                                                                                                                                                                                                                                                      87.9%; Score 687.5; DB 4; Length 228; 93.2%; Pred. No. 3.4e-73; ive 1; Mismatches 6; Indels 3;
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                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 93.2
Matches 136; Conservative
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(PITI/) PITIOT G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-202864/20.
                                                                                                                                                                                                                         antiallergic agents
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                                                                                                                                                                                                                                                Sequence 228 AA;
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The present sequence represents a human odorant binding polypeptide (OBP), designated OBFIG-alpha. OBPS provide long-term retention (gradual release) of lipophilic compounds, so prolong the 'hold' of perfumes, and edeodorants etc. OBP polypeptides are used as binding proteins for decodorants etc. OBP polypeptides are used as binding proteins for hydrophobic ligands (particularly odorants); as competitive inhibitors (agonists or antagonists) of cellular lipocalcin receptors; to detect specific antibodies for diagnosis of allergy, asthma or cancer; for controlling volatilisation of an odorant, specifically in perfumes, commettes or disinfectant compositions; to screen compounds, especially odorants or flavours, e.g. human pheromones, for binding to OBP, also in analysis of complex perfume mixtures; to solubilise lipophilic compounds; for treating hyperlipidemia or obesity, or to supplement non-maternal mix when combined with nutritional fatty acids, as food additives; as a transporter of pharmaceuticals, especially anticancer agents (providing delayed release) but also for delivery across the placental barrier (e.g. placental pathology (rupture of the amnictic membrane); and as
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NLEATFTFWREDRCIQKKILMRKTEEPGKFSAYGGRKLIYLQELPGTDDYVFYCKDQRRG 120
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Pred. No. 2.4e-72;
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23-AUG-2000; 2000US-00649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86.88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.
Matches 130; Conservative
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20-JUN-1997;
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                                                             The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 NLEATFIFMREDRCIQKKILMRKTEEPGKYSACEPLPDPPLPMPNPGCTSPTADGGRKLI 120
                                                                                                                                                                                                                                       diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this spatent did not appear in the printed specification, but was obtained in ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MKTLFLGVTLGLAAALSFTLEEEDITGTWYVKAMVVDKDFPEDRRPRKVSPVKVTALGGG 60
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breast cancer; emphysema; skin disease; reproduction; anti-inflammatory;
antimicrobial.
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responsible for genetic disorders or other traits and to assess biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                          DB 4; Length 221;
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Pred. No. 2.6e-68;
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                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                        Claim 20; SEQ ID NO 42227; 103pp; English
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                                                                                                                                                                                                                                                                                                                                                                                          Query Match 82.7%;
Best Local Similarity 84.8%;
Matches 128; Conservative
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                                                                                                                                                                                                                                                                                                                                                                Sequence 221 AA;
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The present sequence represents a human lipocalin homologue, designated zlipol. The lipocalin homologue, zlipol, is specifically expressed in teestis and mammary gland, particularly breast tumnour tissue. Based on this tissue distribution, zlipol may be used as a diagnostic for breast carcinomas and as a tool for predicting tumour aggressiveness. Agonists can be used for transportation of small hydrophobic molecules either in vivo or in vitro, and so are useful in specifically promoting the growth can be used to identify inhibitors. Zlipol proteins can also be used to prepare antibodies (which can be linked to toxins), and can serve as immunogens. Zlipol proteins can be used as a delivery and encapsulation system to transport and/or stabilise small lipophilic molecules, e.g. to prepare to transport and/or stabilise small lipophilic molecules, e.g. to protect from gut pH and digestive enzymes to modulate their biological control, e.g. to transport retinoids or steroids to receptors, in particular as therapy for breast cancer, emphysema and diseases of the skin. They may also play an important role in reproduction. Other uses include anti-inflammatory responses, and antimicrobial activitiee. Zlipol include anti-inflammatory responses, and antimicrobial activitiee. Zlipol culbible zlipol activity, to derive probes and primers, to derive probes and primers, to derive genetic abnormalities
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                                                                                                               New lipocalin homologue designated zlipol - whose expression is restricted to testis and mammary gland tissues, particularly breast tumour tissue, used to, e.g. predict tumour aggresiveness.
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                                                                                                                                                                                                                                                                                Claim 12; Page 83-84; 94pp; English.
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WPI; 1999-167367/14.
N-PSDB; AAX19505.
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Human; immune related disease; diagnosis; antiinflammatory; cardiant; dermatological; antiarthritic; antirheumatic; immunosuppressive; haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective; antianaemic; hepatotropic; virucide; antipsoriatic; antiallargic; antiallargic; whitasthmatic; systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis; diopathic inflammatory myopathy; Sjogren's syntemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus; whoimmune thrombocytopaenia; immune-mediated renal disease; demyelinating disease; hepatobiliary disease; Whipple's disease; inflammatory bowel disease; gluten-sensitive enteropathy; autoimmune disease; gluten-sensitive enteropathy; mutoimmune disease; transplantation associated disease; mununological disease; transplantation associated disease; graft-versus-host-disease.
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                                                                                                                                                                                                                                                                                                                                                     61 NLEATFTFMREDRCIQKKILMRKTEEPGKFSAYGGRKLIYLQELPGTDDYVFYCKDQRRG 120
                                                                                                  detecting,
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                                                                                                                                                                                                                                                                                                        1 MKTLFLGVTLGLAAALSFTLEEEDITGTWYVKAMVVDKDFPEDRRPRKVSPVKVTALGGG 60
                                                                                              New isolated BS124 polynuclectides and polypeptides - used for detecting diagnosing, preventing or treating diseases or conditions of the breast, such as breast cancer.
                                                                                                                                                                The sequence is that of a BS124-specific epitope. It is useful for detecting, diagnosing, staging, preventing or treating, or determining predisposition to diseases or conditions of the breast, such as breast
                                                                                                                                                                                                                                                                                            1 MKTLFLGVTLGLAAALSFTLEEEDITGTWYVKAMVVDKDFPEDRRPRKVSPVKVTALGGG
                                                                                                                                                                                                                                                                       Gaps
                             Cohen M, Colpitts TL, Friedman PN, Gordon J; es SC, Klass MR, Kratochvil JD, Russell JC, upe SD, Yu H;
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                                                                                                                                                                                                                                             Query Match 79.7%; Score 623; DB 2; Length 170; Best Local Similarity 91.5%; Pred. No. 1.2e-65; Matches 119; Conservative 4; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human PRO1283 protein UNQ653 SEQ ID NO:170.
                                                                                                                                             Disclosure; Page 98-99; 125pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB33450 standard; protein; 170 AA.
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                       Billing-Medel PA, Cohen M,
Granados EN, Hodges SC, K
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                                                                                                                                                                                                                                                                                                                                                                                                   121 GLLHMGKLVG 130
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                                                                           WPI; 1999-105623/09
         (ABBO ) ABBOTT LAB
                                                                                                                                                                                                                           Sequence 170 AA;
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The present invention describes sixty four human PRO proteins which can be used in the treatment of immune related diseases. The human PRO proteins, anti-PRO and ANCS8579 to AACS8642 and AAB33414 to AAB33477 represent human PRO polymucleotide and protein aequences given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sixty four PRO polypeptides, useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosis, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus.
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D, Shelton DL, Smith V;
Wood WI, Yan M;
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                                                                     99WO-US008615.
99US-0131445P.
99US-0132371P.
99US-0134287P.
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99US-0141037P.
99US-0144758P.
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2000WO-US004341
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99US-0146222P
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99WO-US020594
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99WO-US028565
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99US-0123957P
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Kabakoff RC, Lu Y, Pan
Stewart TA, Tumas D, Wa
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30-DEC-1999;
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                                             12-APR-1999;
20-APR-1999;
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 17.5EP-1998,
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22.5EP-1998,
23.5EP-1998,
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                                                                         1 MKTLFLGVTLGLAAALSFTLEEEDITGTWYVKAMVVDKDFPEDRRPRKVSPVKVTALGGG
                                                     Gaps
                                                                                                                                                                                                                                                                                                               Human, PRO polypeptide, membrane bound protein, receptor, diagnosis, transmembrane, secretion; immunoadhesion; pharmaceutical, screening.
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                                Length 170;
                               Query Match 79.7%; Score 623; DB 3; Length 17 Best Local Similarity 91.5%; Pred. No. 1.2e-65; Matches 119; Conservative 4; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                           Human PRO1283 (UNQ653) amino acid sequence SEQ ID NO:162.
                                                                                                                                                                                                                               AAY99389 standard; protein; 170 AA
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98US-0098749P.
98US-0098871P.
98US-0098871P.
98US-0099873E.
98US-0099536P.
98US-0099536P.
98US-0099536P.
98US-0099542P.
98US-0099642P.
98US-0099642P.
98US-0099642P.
98US-00998815P.
98US-0099763P.
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98US-010338P.
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98US-0100683P.
98US-0100684P.
98US-01007110P.
98US-0100711P.
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                                                                                                                                                         GLRYMGKLVG 130
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GLLHMGKLVG 130
             Sequence 170 AA;
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Fong S;
Hillan KJ;
Watanabe CK;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Odorant binding polypeptide; OBP; hydrophobic ligand; odorant; allergy; asthma; cancer; perfume; hyperlipidemia; obesity; food additive; anticancer; foetus detoxification; pregnancy marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Secreted and transmembrane proteins and nucleic acids designated PRO, useful as hybridization probes, in chromosome and gene mapping and gene
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maldi CJ, Gurney AL,
Stewart TA, Tumas D,
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                                                                                                                                                                                                                                                                                                                                                 Baker KP, Botstein D, Desnoyers L, Eaton DL, Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Pan J, Paoni NF, Roy MA, Smith V, Stewart TA Williams PM, Wood WI;
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                                                                                                                                                                                                        30-NOV-1999; 99WO-US028313.
02-DEC-1999; 99WO-US028551.
16-DEC-1999; 99WO-US030095.
05-JAN-2000; 2000WO-US0002196.
                                                                                                                                     99US-0144758P.
99US-0145698P.
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              WO200078961-A1
                                                                                   18-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAA37022 to AAA37144 encode the new isolated human transmembrane, receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The transmembrane and receptor PRO proteins can be used for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions. The polypeptides and nucleotide sequences encoding then have various industrial applications, including uses as pharmaceutical and diagnostic agents. AAA37145 to AAA3730 represent PCR primers and hybridisation probes used in the isolation of the PRO polypeptides from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                             receptor or secreted peptide or small interactions.
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Best Local Similarity 91.5%; Pred. No. 1.2e-65;
Matches 119; Conservative 4; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                          Smith V, Watanabe CK,
                                                                                                                                                                                                                                                                                                                                                                                                                                             New mammalian DNA sequences encoding transmembrane, PRO polypeptides, useful for screening of potential molecule inhibitors of the relevant receptor/ligand
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              98US-0108779P.
98US-010878P.
98US-010878BP.
98US-0108801P.
98US-0108802P.
98US-0108806P.
98US-0108867P.
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GLLHMGKLVG 130
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17-NOV-1998;
17-NOV-1998;
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17-NOV-1998;
17-NOV-1998;
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18-NOV-1998;
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18-NOV-1998;
18-NOV-1998;
18-NOV-1998;
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ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic, antiangiogenic, hypotensive, valnerary and antiarteriosclerotic activities, and can be used in gene therapy. The PRO polynucleotides, proteins, agonists and antagonists are useful for treating or diagnosing
Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary; antiarteriosclerotic; PRO agnosist; PRO antagonist; trauma; gene therapy; cardiovascular disorder; endothelial disorder; cancer; angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension; age-related macular degeneration; arterial restenosis; angina; theumatolid arthritis; myccardial infarction; thrombophlebitis; lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma; wound healing; chromosome mapping; gene mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal.
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2000US-00665350.
2000US-0242922P.
2000US-00709238.
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2001US-00816744.
2001US-00828366.
2001US-00854208.
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2000US-0220664P.
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2000US-00643657.
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2000WO-US023328.
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2000WO-US030873.
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2001US-00796498.
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JF, Watanabe CK,
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                                                                                                                                                                       WO200200690-A2.
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24-OCT-2000;
08-NOV-2000;
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28-FEB-2001;
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05-APR-2001;
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09-MAR-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Godowski
    The present sequence represents a human odorant binding polypeptide (OBP), designated OBPID-alpha. OBPs provide long-term retention (gradual release) of lipophilic compounds, so prolong the 'hold of perfumes, decodorants etc. OBP polypeptides are used as binding proteins for hydrophobic ligands (particularly odorants); as competitive inhibitors (agonists or antagonists) of cellular lipocalin receptors; to detect specific antibodies for diagnosis of allergy, asthma or cancer; for controlling volatilisation of an odorant, specifically in perfumes; cosmetics or disinfectent compositions; to screen compounds, especially odorants or flavours, e.g. human pheromones, for binding to OBP, also in analysis of complex perfume mixtures; to solubilise lipophilic compounds; for treating hyperlipidemia or obesity, or to supplement non-maternal milk when combined with nutritional fatty acids, as food additives; as a transporter of pharmaceuticals, especially anticancer agents (providing for detectival pathology (rupture of the ammiotic membrane); and as
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                                                                                                                                                                                                                                                                                               New human odorant-binding proteins, useful for solubilizing lipophilic compounds in the transportation of anticancer agents or for slow release
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nes 119; Conserv
                                                                                                                                                                                       (PITI/) PITIOT G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 170 AA;
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                                              WO200112806-A2
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                    Ното варіепв.
                                                                                                                                                                                                                                                                                                                            perfumes.
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Paoni NF;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, theumatoid arthritis, angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The PRO polymuclectides have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping, ABL88259 to ABL88267 represent primers and probes used in the exemplification of the present invention
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beneficial mood; hypothalamic; satiety; identification; energy balance;
reproductive biology.
                                                                                                                                                                                                                                                                                                                                                         1 MKTLFLGVTLGLAAALSFTLEEEDITGTWYVKAMVVDKDFPEDRRPRKVSPVKVTALGGG
                                                                                                                                                                                                                                                                                                                                                                                      cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Use of Zlipol or glycodelin (human pheromone polypeptides) for identifying presence of Zlipol receptor, glycodelin receptor, Zlipol ligand or glycodelin ligand in test sample.
                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                    Length 170;
                                                                                                                                                                                                                                                 Score 623; DB 5; Length 1.09 Pred. No. 1.28-65;
                                                                                                                                                                                                                                                                                                                      4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 47-48; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE22099 standard; protein; 170 AA.
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91.5%;
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Matches 119; Conservative
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                                                                                                                                                                                                                            Sequence 170 AA
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                                                                                              Gaps
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0
                                                                 Length 170
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test sample. The present sequence is human Zlipol protein
                                                                                                Indels
                                                              Score 623; DB 5; L
Pred. No. 1.2e-65;
4; Mismatches 7;
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                                                          79.7%;
Best Local Similarity 91.5%;
Matches 119; Conservative 4
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10-MAY-2001; 2001US-00854280.
25-MAY-2001; 2001US-00866028.
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2000US-00664610.
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GLLHMGKLVG 130
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                                    Sequence 170 AA;
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08-NOV-2000;
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14-MAR-2001;
22-MAR-2001;
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                                                                                                                                                                                                                                                                                                                                          The present invention provides the protein and coding sequences of human PRO proteins. These are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder, including cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, mycoardial infarctions, thromopolhebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The present sequence is a PRO protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 NLEATFTFMREDRCIQKKILMRKTBEPGKFSAYGGRKLIYLQELPGTDDYVFYCKDQRRG 120
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                                                                                                                                                                                                                                                                                     One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal.
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                                                                                                                                                                                                                       Goddard A;
                                                                                                                                                                                                                       Gerber H, Gerritsen ME,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABO33631 standard; protein; 170 AA.
                                                                                                                                                                                                                                                                                                                          Claim 11, Fig 206; 567pp; English.
25-MAY-2001; 2001US-00866034.
25-MAY-2001; 2001WO-US017092.
30-MAY-2001; 2001US-00870574.
30-MAY-2001; 2001WO-US017443.
01-UJN-2001; 2001WO-US017800.
20-JUN-2001; 2001WO-US019692.
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Stephan JF, Watanabe CK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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Matches 119; Conservative
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                                                                                                           GODDARD A.
GODOWSKI P J.
GURNEY A L.
HILLAN K J.
MARSTERS S A.
                                                                                         GERBER H.
GERRITSEN M E.
                                                                 GENENTECH INC.
                                                                                                                                                       PAN J.
PAONI N F.
STEPHAN J F.
WATANABE C K.
WILLIAMS P M.
                                                                                                                                                                                                                        Ferrara N,
                                                                                                                                                                                                                                                            WPI; 2002-171999/22.
                                                                         BAKER K P.
FERRARA N.
                                                                                                                                                                                                                                                                     N-PSDB; ABL95663.
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                                                                                                                                                       (PANJ/) F
(PAON/) F
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Human; secreted and transmembrane protein; PRO; angiogenesis; endothelial cell proliferation; wound healing; immune response; T-lymphocytes proliferation; neonatal heart hypertrophy; tumour; cardiac insufficiency disorder; calcium flux; inflammation; vascular endothelial growth factor-stimulated proliferation; mammalian kidney mesangial cell proliferation; Berger disease; nephropathy; Schanlein-Henoch purpura; cellac disease; crohn's dermatitis herperiformis; diabetes; haemoglobin switch; insulinaemia; pancreatic beta-cell precursor cell differentiation; thalassemias; obesity; auditory hair cell regeneration; hearing loss; bone disorder; cartilage disorder; sports injury; arthritis.
Novel human secreted and transmembrane protein PRO1283.
                                                                                                                                                                                                                                                                                                                                                                                                  98US-0098716P.
98US-0098723P.
98US-0098723P.
98US-0098723P.
98US-0098723P.
98US-009873P.
98US-009973P.
98US-0099742P.
98US-0099742P.
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98US-0099742P.
98US-0099743P.
98US-0099763P.
98US-0099763P.
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98US-0101741P.
98US-0101915P.
98US-0101916P.
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9805-0102240P-
9805-0102340P-
9805-0102310P-
9805-0102311P-
9805-0102311P-
9805-0102511P-
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 29-SEP-1998, 29-SEP-1998, 29-SEP-1998, 29-SEP-1998, 29-SEP-1998, 30-SEP-1998, 30-SE
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-NOV-1998;
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Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
Williams PM, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel igolated PRO polypeptides e.g. PRO1130, PRO1275, PRO1418, PRO1555, PRO1787 that modulate glucose or free fatty acid uptake by skeletal muscle cells, and are useful for treating diabetes, hyper- or hypo-
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Best Local Similarity 91.5%; Pred. No. 1.2e-65;
Matches 119; Conservative 4; Mismatches 7; Indels
16-APR-1999; 99WO-US000106.
16-APR-1999; 99US-0141037P.
20-JUL-1999; 99US-0144758P.
20-JUL-1999; 99US-0144758P.
21-JUL-1999; 99WO-US020111.
15-SEP-1999; 99WO-US020111.
15-SEP-1999; 99WO-US020111.
16-DEC-1999; 99WO-US02113.
02-DEC-1999; 99WO-US021851.
16-DEC-1999; 99WO-US02851.
16-DEC-1999; 99WO-US02851.
16-DEC-1999; 99WO-US02851.
16-DEC-1999; 99WO-US028851.
16-DEC-1999; 99WO-US028851.
11-FEB-2000; 2000WO-US002851.
22-MAR-2000; 2000WO-US00376.
11-MAR-2000; 2000WO-US00884.
11-MAY-2000; 2000WO-US014042.
22-MAY-2000; 2000WO-US014941.
23-MUS-2000; 2000WO-US014941.
23-MUS-2000; 2000WO-US012564.
23-MUS-2000; 2000WO-US012564.
23-MUS-2000; 2000WO-US012564.
23-MUS-2000; 2000WO-US012564.
23-MUS-2000; 2000WO-US012666.
01-UNN-2001; 2001WO-US012678.
29-UNN-2001; 2001WO-US019692.
29-UNN-2001; 2001WO-US011735.
04-SEP-2001; 2001WO-US011735.
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GLLHMGKLVG 130
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N-PSDB; ACD68350.
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1: \( \cgn2 \frac{6}\) \text{prodata} \\ \text{Jubbaa}\\ \text{USO7}\) \text{PUBCOMB.pep:*} \\
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Description	Sequence 22, App]	Sequence 2, Appl:	Sequence 162, App	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
SUMMARIES	US-09-099-823-22	JS-09-951-845-2	JS-09-946-374-162	JS-10-006-856A-162	US-10-006-818A-162	US-10-006-485A-162	US-10-013-907A-162	US-10-015-499A-162	US-10-015-393A-162	.015-869A-162	US-10-012-121A-162	-006-116A-162
SUM	0-60-SN	0S-09-5	-60-SD	US-10-	US-10-	US-10-	US-10-	US-10-	US-10-	US-10-	US-10-	US-10-
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& Query Match	7.67	79.7	79.7	79.7	79.7	79.7	79.7	79.7	79.7	79.7	79.7	79.7
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Sequence 162, 623 79.7 170 14 US-10-013-430A-162 Sequence 162, 623 79.7 170 14 US-10-013-430A-162 Sequence 162, 623 79.7 170 14 US-10-012-386A-162 Sequence 162, 623 79.7 170 14 US-10-012-386A-162 Sequence 162, 623 79.7 170 14 US-10-023-084-206 Sequence 162, 623 79.7 170 14 US-10-223-084-206 Sequence 206, 623 79.7 170 14 US-10-011-692A-162 Sequence 162, 623 79.7 170 14 US-10-013-391A-162 Sequence 162, 623 79.7 170 14 US-10-015-391A-162 Sequence	623 79.7 170 14 US-10-017-527A-162 Sequence 162, 623 79.7 170 14 US-10-017-527A-162 Sequence 162, 623 79.7 170 14 US-10-013-913A-162 Sequence 162, 623 79.7 170 14 US-10-013-430A-162 Sequence 162, 623 79.7 170 14 US-10-013-430A-162 Sequence 162, 623 79.7 170 14 US-10-015-386A-162 Sequence 162, 623 79.7 170 14 US-10-015-386A-162 Sequence 162, 623 79.7 170 14 US-10-023-084-206 Sequence 206, 623 79.7 170 14 US-10-223-084-206 Sequence 206, 623 79.7 170 14 US-10-011-692A-162 Sequence 162, 623 79.7 170 14 US-10-011-692A-162 Sequence 162, 623 79.7 170 14 US-10-012-692A-162 Sequence 162, 623 79.7 170 14 US-10-011-692A-162 Sequence 162, 623 79.7 170 14 US-10-013-918-162 Sequence 162, 623 79.7 170 14 US-10-013-918-162 Sequence 162, 623 79.7 170 14 US-10-013-918-162 Sequence 162, 623 79.7 170 14 US-10-015-918-162 Sequence 162, 623 79.7 170 14 US-10-015-918-918-918-918-918-918-918-918-918-918	623 79.7 170 14 US-10-017-527A-162 Sequence 162, 623 79.7 170 14 US-10-013-918A-162 Sequence 162, 623 79.7 170 14 US-10-015-386A-162 Sequence 162, 623 79.7 170 14 US-10-015-386A-162 Sequence 162, 623 79.7 170 14 US-10-015-386A-162 Sequence 162, 623 79.7 170 14 US-10-223-084-206 Sequence 206, 623 79.7 170 14 US-10-011-692A-162 Sequence 162, 623 79.7 170 14 US-10-011-692A-162 Sequence 162, 623 79.7 170 14 US-10-020-063A-162 Sequence 162, 623 79.7 170 14 US-10-020-063A-162 Sequence 162, 623 79.7 170 14 US-10-020-063A-162 Sequence 162, 623 79.7 170 14 US-10-011-833A-162 Sequence 162, 623 79.7 170 14 US-10-015-391A-162 Sequen

APPLICANT: HODGES, STEVEN C.
APPLICANT: HODGES, STEVEN C.
APPLICANT: KRASS, MICHAEL R.
APPLICANT: KRATCHVIL, JON D.
APPLICANT: SCHEFFEL, OHN C.
APPLICANT: STROUPE, STEPHEN D.
APPLICANT: STROUPE, STEPHEN D.
APPLICANT: STROUPE, STEPHEN D.
APPLICANT: YU, HODE,
STROUPE, STEPHEN D.
APPLICANT: YU, HODE,
TITLE OF INVENTION: FOR DETECTING DISEASES OF THE BREAST
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDOLT LAKE. COUNTRY: USA
ZIP: 60064-3500
COMPUTER READMALE DISKette
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/099,823 NG-MEDEL, PATRICIA STREET: 100 Abbott Park Road CITY: Abbott Park Road STATE: 11. RESULT 1
US-09-09-023-22
Sequence 22, Application US/09099823
Patent No. US20020018990A1
GENERAL INFORMATION
APPLICANT: COHEW, MAURICE COHEN, MAURICE COLPTIS, TRACEY L. FRIEDMAN, PAULA N. APPLICANT: APPLICANT: APPLICANT:

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Sequence 162, Application US/09946374 Publication No. US20030073129A1
                                                                                                                                                                                                           Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth J.
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Eaton, Dan L.
Ferrara, Napoleone
Fong, Sherman
Gao, Wei-Qiang
Goddard, Audrey
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Stewart, Timothy A.
                                                                                                                                                                                                                                                                 Pan, James
Paoni, Nicholas F.
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                                                                                                     APPLICANT: Baker, Kevin P. APPLICANT: Botstein, David
121 GLLHMGKLVG 130
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                                                                                         GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                        Query Match 79.7%; Score 623; DB 9; Length 17
Best Local Similarity 91.5%; Pred. No. 1.6e-62;
Matches 119; Conservative 4; Mismatches 7; Indels
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Patent No. US20020098497A1
GENERAL INFORMATION:
APPLICANT: Lok, S1
APPLICANT: Foster, Donald C.
APPLICANT: Holloway, James L.
TILE OF INVENTION: Use of Human Phermone Polypeptides
FILE REFERENCE: 00-85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Mismatches
        CLASSIFICATION:
PRIOR APPLICATION DATA:
PPLICATION NUMBER: 08/879,354
PTLING DATE: 20-UN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFONE: 847/938-1729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/951,845
CURRENT FILING DATE: 2001-09-12
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                     ; TOPOLOGY: linear
; MOLECULE TYPE: No. US20020018990Ale
US-09-099-823-22
                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids
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Best Local Similarity 91.5'
Matches 119; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: si
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LENGTH: 170
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REIOR PELICA DATE: 1998-09-10
REIOR PLICATION NUMBER: 60/100395
RRIOR FILING DATE: 1998-09-15
RRIOR FILING DATE: 1998-09-15
RRIOR FILING DATE: 1998-09-15
RRIOR FILING DATE: 1998-09-16
RRIOR APPLICATION WUMBER: 60/100661
RRIOR APPLICATION WUMBER: 60/100661
RRIOR APPLICATION NUMBER: 60/100664
RRIOR RELIAGATION NUMBER: 60/100664
RRIOR RELIAGATION NUMBER: 60/100694
RRIOR RELIAGATION NUMBER: 60/100694
RRIOR RELIAGATION NUMBER: 60/100919
RRIOR FILING DATE: 1998-09-17
RRIOR RELIAGATION NUMBER: 60/100919
RRIOR RELIAGATION NUMBER: 60/101014
RRIOR RELIAGATION NUMBER: 60/101014
RRIOR RELIAGATION NUMBER: 60/101014
RRIOR RELIAGATION NUMBER: 60/101018
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CURRENT FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: 60/098716
PRIOR FILING DATE: 1998-09-01
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PRIOR PELING DATE: 1998-09-01
PRIOR PELING DATE: 1998-09-01
PRIOR PELING DATE: 1998-09-01
PRIOR FILING DATE: 1998-09-01
PRIOR PILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098750
PRIOR PELING DATE: 1998-09-02
PRIOR FILING DATE: 1998-09-09
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Eaton, Dan 1.
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                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-006-818A-162
                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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                                                                                                                                             LENGTH: 170
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                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Pani, James
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2830PIC14
CURRENT APPLICATION NUMBER: US/10/006,856A
CURRENT FILING DATE: 2002-05-10
NUMBER OF SEQ ID NOS: 477
Prior Application removed - See File Wrapper or Palm
SEQ ID 0162
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APPLICANT: Paoni, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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US-10-006-818A-162
; Sequence 162, Application US/10006818A
; Publication No. US20030054406A1
; GENERAL INFORMATION:
; APPLICANT: Botstein, David
                                                                                                                     Sequence 162, Application US/10006856A Publication No. US20030044841A1
PUBLICATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Besterin, David
APPLICANT: Desnoyers, Luc
APPLICANT: Besnoyers, Luc
APPLICANT: Eaton, Dan 1.
                                                                                                                                                                                                                                                                                                                                                      Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth J.
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth J.
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Eaton, Dan 1.
Ferrara, Napoleone
Fong, Sherman
Gao, Wel-Qiang
Goddard, Audrey
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Fong, Sherman
Gao, Wei-Qiang
Goddard, Audrey
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Best Local Similarity 91.5%;
Matches 119; Conservative
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121 GLLHMGKLVG 130
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; ORGANISM: Homo sapiens
US-10-006-856A-162
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61 NLEATFTFMREDRCIOKKILMRKTEEPGKFSAYGGRKLIYLQELPGTDDYVFYCKDQRRG 120
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APPLICANT: Paoni, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2830PIC9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MKTLFLGVTLGLAAALSFTLEEEDITGTWYVKAMVVDKDFPEDRRPRKVSPVKVTALGGG
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Pred. No. 1.6e-62;
4; Mismatches 7; Indels
TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2830P1C4
CURRENT APPLICATION NUMBER: US/10/006,818A
CURRENT FILING DATE: 2001-12-06
PLIOR APPLICATION removed - See File Wrapper or Palm Pumber OF SEQ ID NOS: 477
SEQ ID NO 162
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Fong, Sherman
Gao, Wei-Qiang
Goddard, Audrey
Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth J.
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NUMBER: 60/099602	R: 6	1998-09-09 NUMBER: 60/099741	: 1998-09-10	-09-10	NUMBER: 60/099763 : 1998-09-10	0 -	1998-09-10 NUMBER: 60/099808	1998-09-10 NIMBER: 60/099812	10	NUMBER: 60/099815 1998-09-10	ER: 60	1998-09-10 NUMBER: 60/100385	1998-	9-15	NUMBER: 60/100390 1998-09-15	NUMBER: 60	1998- NUMBER	1998-09-16	NUMBER: 60/100661	NUMBER: 6	1998-	1998-09-16	NUMBER: 60/100683 1998-09-17	NUMBER:	NUMBER: 6	1998-	1998-09-17	1998-09-18	NUMBER: 60 1998-09-1	NUMBER:	NUMBER: 6	LYYB-09-1 NUMBER: 60	1998- NUMBER	1998-09-	1998-09-18	NUMBER: 60/101279 : 1998-09-22	NUMBER: 60	1998-0 NUMBER:	1998-09-	1998-09-23	NUMBER: 60/101475 : 1998-09-23	NUMBER: 60	9.6	: 1998-09-23 NUMBER: 60/101479	
APPLICATION PILING DATE:	PPLICATION	ILING DATE PPLICATION	ILING DATE	ILING DATE	APPLICATION FILING DATE:	PPLICATION	PPLICATION	FILING DATE:	ILING DATE	ATION	ATION	ATION	FILING DATE:	DATE	DATE	ATION	DATE	DATE	TATION	ATION	3 DATE	DATE	DATE	ATION	CATION	3 DATE	G DATE	DATE	TION	APPLICATION	APPLICATION 1	FILING DATE: APPLICATION	FILING DATE: APPLICATION	FILING DATE:	FILING DATE:	APPLICATION FILING DATE:	APPLICATION	FILING DATE APPLICATION	FILING DATE	FILING DATE	APPLICATION FILING DATE	APPLICATION	CATI	FILING DATE APPLICATION	
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PRIOR FILING DATE: 1996-09-23

PRIOR PILING DATE: 1996-09-24

PRIOR APPLICATION NUMBER: 60/101741

PRIOR PILING DATE: 1998-09-24

PRIOR PILING DATE: 1998-09-24

PRIOR PILING DATE: 1998-09-24

PRIOR PILING DATE: 1998-09-24

PRIOR PILING DATE: 1998-09-29

PRIOR PILING DATE: 1998-09-30

PRIOR PILING DATE: 1998-10-07

PRIOR PILING DATE: 1998-10-10

PRIOR PILING DATE: 1998-10-10

PRIOR PILING DATE: 1998-10-10

PRIOR PILING DATE: 1998-10-10

PRIOR PILING DATE: 1998-1

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SEQ ID NO 162
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APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2830PLC34
CURRENT APPLICATION NUMBER: US/10/013,907A
CURRENT FILING DATE: 2001-12-10
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 477
SEQ ID NO 162
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PRIOR APPLICATION NUMBER: 60/105693
PRIOR FILING DATE: 1998-10-26
PRIOR FILING DATE: 1998-10-26
PRIOR FILING DATE: 1998-10-26
PRIOR APPLICATION NUMBER: 60/105807
PRIOR APPLICATION NUMBER: 60/10581
PRIOR APPLICATION NUMBER: 60/10581
PRIOR PILING DATE: 1998-10-27
PRIOR PILING DATE: 1998-10-27
PRIOR APPLICATION NUMBER: 60/10682
PRIOR APPLICATION NUMBER: 60/106023
PRIOR FILING DATE: 1998-10-27
PRIOR APPLICATION NUMBER: 60/106023
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth J.
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APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan 1.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
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GLLHMGKLVG 130
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US-10-013-907A-162
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61 NLEATFIFMREDRCIOKKILMRKTEEPGKFSAYGGRKLIYLQELPGTDDYVFYCKDQRRG 120
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APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Pan, James
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2830P1C42
CURRENT APPLICATION NUMBER: US/10/015,499A
CURRENT FILING DATE: 2001-12-11
Prior Application removed - See File Wrapper or Palm
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Publication No. US20030069179A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Benoyers, Luc
APPLICANT: Perrara, Napoleone
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Fong, Sherman
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Autrey
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
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APPLICANT: Batetin, David
APPLICANT: Besnoyers, Luc
APPLICANT: Eaton, Dan 1.
APPLICANT: Ferrara, Napoleone
APPLICANT: Forg, Sherman
APPLICANT: Goo, Wei-Qiang
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
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Matches 119; Conservative
                               121 GLLHMGKLVG 130
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121 GLLHMGKLVG 130
121 GLRYMGKLVG 130
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; ORGANISM: Homo sapiens
US-10-015-499A-162
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61 KLEATFTFMREDRCIQKKILMRKTEEPGKYSAYGGRKLMYLQELPRRDHYIFYCKDQHHG 120
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Eaton, Dan 1.
Ferrara, Napoleone
Fong, Sherman
Gao, Wei-Qiang
Goddard, Audrey
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Fong, Sherman
Gao, Wei-Qiang
Goddard, Audrey
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Best Local Similarity 91.5%;
Matches 119; Conservative
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Hillan, Kenneth J.
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Hillan, Kenneth J
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Desnoyers, Luc
Eaton, Dan 1.
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APPLICANT: Botstein, David
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CURRENT APPLICATION NUMBER: US/10/015,869A
CURRENT FILING DATE: 2002-06-25
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 477
SEQ ID NO 162
                                                                                                                                                                                                                                                                                                                        1 MKTLFLGVTLGLAAALSFTLEEEDITGTWYVKAMVVDKDFPEDRRPRKVSPVKVTALGGG
                   TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REPERENCE: P2839DLC46 CURRENT APPLICATION NUMBER: 105/015,393A CURRENT FILING DATE: 2002-06-10
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Pred. No. 1.6e-62;
4; Mismatches 7; Indels
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                                                                                                         Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 477
SEQ ID NO 162
LENGTH: 170
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Pred. No. 1.6e-62;
4; Mismatches 7;
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Grimaldi, Christopher
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Fong, Sherman
Gao, Wei-Qiang
Goddard, Audrey
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Best Local Similarity 91.5%;
Matches 119; Conservative '
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Best Local Similarity 91.5%;
Matches 119; Conservative
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Hillan, Kenneth J.
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Paoni, Nicholas F.
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Desnoyers, Luc
Eaton, Dan 1.
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                                                                                                                                                                                                                                                                                                                                             APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2830PIC20
CURRENT APPLICATION NUMBER: US/10/012,121A
CURRENT FILING DATE: 2001-12-07
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Pred. No. 1.6e-62;
4; Mismatches 7; Indels
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SEQ ID NO 162
LENGTH: 170
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; sequence 162, Application US/10012121A; Publication No. US20030073810A1; GENERAL INFORMATION:
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Grimaldi, Christopher J.
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Grimaldi, Christopher J.
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PRIOR APPLICATION NUMBER: 60/100919
PRIOR FILING DATE: 1998-09-18
PRIOR PLILING DATE: 1998-09-17
PRIOR PLILING DATE: 1998-09-17
PRIOR PLILING DATE: 1998-09-17
PRIOR PLILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/101014
PRIOR PLILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 60/101014
PRIOR PLILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 60/101071
PRIOR PLILING DATE: 1998-09-18
PRIOR PLILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 60/101741
PRIOR PLILING DATE: 1998-09-24
PRIOR PLILING DATE: 1998-09-24
PRIOR PLILING DATE: 1998-09-24
PRIOR PLILING DATE: 1998-09-29
PRIOR PLILING DATE: 1998-09-29
PRIOR APPLICATION NUMBER: 60/10207
PRIOR PLILING DATE: 1998-09-29
PRIOR PLILING DATE: 1998-09-30
PRI
APPLICANT: Pun. James

APPLICANT: Pun. James

APPLICANT: Pun. James

TITLE OF INVESTOR: Secreted and Transmeabrane Polypeptides and Mucleic TITLE OF INVESTOR: Secreted and Transmeabrane Polypeptides and Mucleic TITLE OF INVESTOR: Secreted and Transmeabrane Polypeptides and Mucleic TITLE OF INVESTOR: 2001-12-16

PURCHARNT PELINGANDER: 2001-12-16

PRICE PLICATION NUMBER: 60/09373

PRICE PLICATION NUMBER: 60/09373

PRICE PLICATION NUMBER: 60/09374

PRICE PLICATION NUMBER: 60/09374

PRICE PLICATION NUMBER: 60/09376

PRICE PLICATION NUMBER: 60/10376

PRICE PLICATION NUMBER: 60/10376
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APPLICATION NUMBER: 60/100848
FILING DATE: 1998-09-18
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APPLICANT: Hillan, Kenneth J.

APPLICANT: Pan, James
APPLICANT: Pan, Unicholas F.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2830PLC13
CURRENT APPLICATION NUMBER: US/10/006,117A
CURRENT FILING DATE: 2002-03-19
PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 477
SEQ ID NO 162
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IITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
IITLE OF INVENTION: Acids Encoding the Same
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Pred. No. 1.6e-62;
4; Mismatches 7;
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PRIOR PELING DATE: 1998-09-01
PRIOR PELICATION NUMBER: 60/098750
PRIOR PELING DATE: 1998-09-01
PRIOR PELING DATE: 1998-09-01
PRIOR PELING DATE: 1998-09-02
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Fong, Sherman
Gao, Wei-Qiang
Goddard, Audrey
Godowski, Paul J.
Grimaldi, Christopher J
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Hillan, Kenneth J
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APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan 1.
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121 GLLHMGKLVG 130
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CORGANISM: Homo sapiens
US-10-006-117A-162
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Best Local Similarity
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Pred. No. 1.6e-62;
4; Mismatches 7;
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Sequence 162, Application US/10006117A
PUBLICANT NO. US20030082627A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Bestein, David
APPLICANT: Eaton, Dan 1.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wel-Olang
APPLICANT: Goddard, Audrey
                                                                                                                                                                 PRIOR FILING DATE: 1998-10-07
PRIOR APPLICATION NUMBER: 60/10349
PRIOR APPLICATION NUMBER: 60/103449
PRIOR PLING DATE: 1998-10-06
PRIOR PELING DATE: 1998-10-08
PRIOR FILING DATE: 1998-10-08
PRIOR FILING DATE: 1998-10-08
PRIOR PILING DATE: 1998-10-08
PRIOR APPLICATION NUMBER: 60/103679
PRIOR APPLICATION NUMBER: 60/103711
PRIOR APPLICATION NUMBER: 60/10457
PRIOR PILING DATE: 1998-10-08
PRIOR PILING DATE: 1998-10-08
PRIOR PILING DATE: 1998-10-09
PRIOR PILING DATE: 1998-10-20
PRIOR PILING DATE: 1998-10-22
PRIOR PILING DATE: 1998-10-26
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Grimaldi, Christopher J.
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APPLICATION NUMBER: 60/106023
FILING DATE: 1998-10-28
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Best Local Similarity 91.5%;
Matches 119; Conservative
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GLLHMGKLVG 130
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PRIOR APPLICATION NUMBER: 60/101479
PRIOR FILING DATE: 1998-09-23
PRIOR PILING DATE: 1998-09-23
PRIOR PILING DATE: 1998-09-24
PRIOR PILING DATE: 1998-09-29
PRIOR PILING DATE: 1998-09-30
PRIOR PILING DATE: 1998-10-07

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79.7%; Score 623; DB 14;
Best Local Similarity 91.5%; Pred. No. 1.6e-62;
Matches 119; Conservative 4; Mismatches 7;
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APPLICANT: Botstein, David
APPLICANT: Besnoyers, Luc
APPLICANT: Eston, Dan 1.
APPLICANT: Ferrara, Napoleone
APPLICANT: Food, Wei-Oiang
APPLICANT: Good, Wei-Oiang
APPLICANT: Goddwski, Paul J.
APPLICANT: Goddwski, Paul J.
APPLICANT: Grimaldi, Christopher J.
PRIOR FILING DATE: 1998-10-21
PRIOR APPLICATION NUMBER: 60/105169
PRIOR PILING DATE: 1998-10-22
PRIOR PILING DATE: 1998-10-22
PRIOR PPLING DATE: 1998-10-22
PRIOR APPLICATION NUMBER: 60/105693
PRIOR PILING DATE: 1998-10-26
PRIOR PILING DATE: 1998-10-26
PRIOR APPLICATION NUMBER: 60/105694
PRIOR APPLICATION NUMBER: 60/105694
PRIOR APPLICATION NUMBER: 60/105807
PRIOR PILING DATE: 1998-10-27
PRIOR PILING DATE: 1998-10-27
PRIOR PILING DATE: 1998-10-27
PRIOR PILING DATE: 1998-10-27
PRIOR APPLICATION NUMBER: 60/105812
PRIOR APPLICATION NUMBER: 60/105812
PRIOR PILING DATE: 1998-10-27
PRIOR PILING DATE: 1998-10-27
PRIOR PILING DATE: 1998-10-27
PRIOR PILING DATE: 1998-10-27
PRIOR PILING DATE: 1998-10-28
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Best Local Similarity 91.5
Matches 119; Conservative
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121 GLLHMGKLVG 130
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1 MKTLFLGVTLGLAAALSFTLEEEDITGTWYVKAMVVDKDFPEDRRPRKVSPVKVTALGGG-60

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GenCore version 5.1.6
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OM protein - protein search, using sw model

June Run on:

7, 2005, 14:30:34 ; Search time 39 Seconds (without alignments) 360.196 Million cell updates/sec

US-10-049-372-4 782

1 MKTLFLGVTLGLAAALSFTL......KLVGPCRCPHVGSPGHLTCR 146 score: Title: Perfect so Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched: 283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMARIES	
		dР				
Result No.	Score	Query Match	Length	DB	ID	Description
				!		
-	284.5	36.4	1/6	7	A40464	odor and punding pr
7	274.5	35.1	176	-	LCHUL	lacrimal lipocalin
m	239	30.6	177	~	S43647	von Ebner's gland
4	238.5	30,5	176	7	JC6503	tear lipocalin von
ď	232	29.7	177	~	S08161	hydrophobic molecu
9	205	26.2	185	7	S51803	vomeronasal secret
7	186.5	23.8	176	7	A33672	late lactation pro
60	171	21.9	182	7	S51802	vomeronasal secret
6	138	17.6	85	~	A28561	ä
10	122	15.6	183	8	\$25465	lipocalin - giant
11	120.5	15.4	184	7	S52354	gene cpl-1 protein
12	118	15.1	162	7	S33876	beta-lactoglobulin
13	108.5	13.9	155	~	A29699	beta-lactoglobulin
14	107	13.7	180	Н	LGGT	beta-lactoglobulin
15	106.5	13.6		N	S33877	beta-lactoglobulin
16	105	13.4	163	7	S11538	beta-lactoglobulin
17	102	13.0		~	S33878	beta-lactoglobulin
18	101	12.9	180	Н	LGSH	beta-lactoglobulin
19	66	12.7		-	LGBO	beta-lactoglobulin
20	66	12.7		~	A45542	beta-lactoglobulin
21	96.5	12.3		N	S14719	beta-lactoglobulin
22	96.5	12.3		Н	LGH02	beta-lactoglobulin
23	96	12.3	180	Н	A39167	placental protein
24	93.5	12.0		~	S33875	beta-lactoglobulin
25	89.5	11.4		٦	OVFGP	olfactory protein
56	89	11.4	162	٦	LGBUI	beta-lactoglobulin
27	89	11.4		7	800132	beta-lactoglobulin
28	89	11.4	188	Н	SQRTAD	androgen-dependent
29	88	11.3	178	0	A30230	quiescence-specifi

odorant-binding pr beta-lactoglobulin beta-lactoglobulin	hypothetical prote butyrl-Coa dehydr DNA primase - phag phosphoribulokinas	F7A19.16 protein - prostaglandin D sy hypothetical prote 3,4-dihydroxy-2-bu Mg(2+) chelatase f	hypothetical prote 3,4 dihydroxy-2-bu 3,4 dihydroxy-2-bu hypothetical prote
A28713 LGHOD LGHO	T35594 T45286 C41830 JQ0400	B86274 S57748 T27820 A38159 AD3501	T15091 A85965 A98120 S74044
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172 162 162	233 379 777 292	537 189 611 252 339	604 217 217 337
10.9 10.7 10.5	10.2 10.1 9.7	ഥ. ന. ന. ന. ത. ത. ത. ത. ത	9000
88 84 82	79.5 79 76 75	74.5 73 72.5 72.5	72 71.5 71.5 71.5 71.5
30 31 32	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	37 38 44 40 10	1444 12643

ALIGNMENTS

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C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-May-1992 #sequence_revision 28-May-1992 #text_change 09-Jul-2004
C;Accession: A40464
R;Dear, T.N.; Campbell, K.; Rabbitts, T.H.
Biochemistry 30, 10376-10382, 1991
A;Title: Molecular cloning of putative odorant-binding and odorant-metabolizing protein A;Reference number: A40464; MUID:92031476; PMID:1931961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
A40464 odorant-binding protein homolog OBP-II precursor - rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 36.4%; Score 284.5; DB 2; I Similarity 44.4%; Pred. No. 2e-21; 60; Conservative 21; Mismatches 49;
                                                                                                                                                                                                                                                   A,Accession: A40464
A,Status: preliminary
Mnolecule type: mRNA
A,Residues: 1-176 < DEA>
A,Cross-references: UNIPROT: 063613; GB:M76733
CS.Operfamily: lipocalin; lipocalin homology
F;25-171/Domain: lipocalin homology < LIP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 60; Conserv
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22 1 MKTLFLGV-TLGLAAALSFTL----BEEDITGTWYVKAMVVDKDFPEDRRPRKVSPVKVT d ઠે

56 ALGGGNLEATFTFMREDRCIQKKILMRKTEEPGKFSAYGGRKLIYLQELPGTDDYVFYCK 115 || ||:|| || : | : | || ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| | ð 셤

116 DORRGGLRYMGKLVG 130 121 GORHGKSYLKGKLVG 135 ò 셤

Discrimal lipocalin precursor - human
NiAlternate names: lipocalin 1; PMFA; tear prealbumin; von Ebner's gland protein
C;Species: Home sapiens (man)
C;Date: 10-Jun-1993 #sequence revision 02-Jun-1995 #text change 09-Jul-2004
C;Accession: A44029, A49186; \$29842; 153728; \$18929; \$34277
R;Redl, B.; Holzfeind, P.; Lottspeich, F.
A;Redl, Chem. 2577, 20282-20287, 1992
A;Pitle: CDNA cloning and sequencing reveals human tear prealbumin to be a member of th

A;Cross-references: UNIPROT:P31025; GB:M90424; NID:g642380; PIDN:AAA61845.1; PID:g18445 A;Experimental source: lacrimal gland, tears A;Note: sequence extracted from NCBI backbone (NCBIN:115716, NCBIP:115717) A; Molecule type: mRNA; protein A; Residues: 1-176 < RED>

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A;Note: part of this sequence, including the amino end of the mature protein, were deterable by those: 22-tea and 24.8er, were also observed as amino-terminal residues
R;Lassagne, H.; Gachon, A.M.

B;Lassagne, H.; Gachon, A.M.

A;Pitle: Cloning of a human lacrimal lipocalin secreted in tears.

A;Accession: A49186; MUID:93122888; PMID:8500570

A;Accession: A49186

A;Accession: A29186

A;Accession: A29186

A;Accession: A29186

A;Accession: A29186

A;Accession: B20497

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Cispecies: Rattus norvegicus (Norway rat)
Cispecies: Rattus norvegicus (Norway rat)
Cispecies: O-Oct-1994 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
Cispecies: Cisco-Oct-1994 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
Cispecies: Cisco-Oct-1994 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
Ricock, K.; Ahlers, C.; Schmale, H.
Ricock, K.; Ahlers, C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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42.3%; Pred. No. 2e-20;
tive 27; Mismatches 41;
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nes 58; Conservative
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A;Cross-references: UNIPROT:P41244; GB:X74806; NID:g505302; PIDN:CAA52810.1; PID:g505303
C;Superfamily: lipocalin; lipocalin homology
F;25-172/Domain: lipocalin homology <LIP>
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Cispecies: Rattus norvegicus (Norway rat)
Cispecies: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
CiAccession: 808161; 843648
Rischmale, H.; Holtgreve-Grez, H.; Christiansen, H.
Rature 343, 366-369, 1990
Aitle: Possible role for salivary gland protein in taste reception indicated by homolc A;Reference number: 808161; MUID:90136923; PMID:1689010
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A;Residues: 1-177 <SCH>
A;Cross-references: UNIPROT:P20289; GB:X52016; GB:X62419; NID:g57473; PIDN:CAA36263.1; P
                                                                                                                                                                                                                                                                                                                                                                                              61 KTLEGGNLQVKFTVLISGRCQEMSTVLEKTDEPGKYTAYSGKQVVYSIPSAVEDHYIFYY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53 KVTALGGGNLEATFTFMREDRCIQKKILMRKTEEPGKFSAYGGRKLIYLQELPGTDDYVF 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55 TALGGGNLEATFTFWREDRCIOKKILMRKTEEPGKFSAYGGRKLIYLQELPGTDDYVFYC 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tear lipocalin von Ebner's gland protein - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                           1 MKTLFLGVTLGLAAALSFTLEE-----BDITGTWYVKAMVVDKDFPEDRRPRKVSPV
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                                                                                                                                                                                                                                               1 MKTLFLGVTLGLAAALS----FTLEEEDITGTWYVKAMVVDKDFPEDR-RPRKVSPVKV
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                                                                                                                         Length 177;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene 202, 61-67, 1997
A;Title: Structure and organization of the porcine LCN1
A;Reference number: JC6503; MUID:98087418; PMID:9427546
A;Accession: JC6503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
                                                                                                                         Query Match 30.6%; Score 239; DB 2; Best Local Similarity 37.1%; Pred. No. 8.1e-17; Matches 53; Conservative 28; Mismatches 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30.5%; Score 238.5; DB 2
36.2%; Pred. No. 9.1e-17;
tive 30; Mismatches 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C, Accession: JC6503
R, Holzfeind, P.; Merschak, P.; Wojnar, P.; Redl, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT: P53715; GB:U96150
C;Superfamily: lipocalin; lipocalin homology
F;27-171/Domain: lipocalin homology <LIP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   115 KDORRGGLRYMGKLVGPCRCPHV 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 EGKIHRHHFQIAKLVG--RNPEI 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Residues: 1-176 < HOL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: S08161
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Local Sim
50;
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9

Gaps

6

54; Indels

DB 2; Length 176;

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C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
C;Accession: $51802
R;Miyawaki, A.; Matsushita, F.; Ryo, Y.; Mikoshiba, K.
BMBO J. 13, 5835-5842, 1994
A;Title: Possible pheromone-carrier function of two lipocalin proteins in the vomeronas A;Reference number: $51802
A,Accession: $51802
A,Scatus: preliminary; nucleic acid sequence not shown
A;Rolecule type: mRNA
A;Residues: 1-182 <MIXA
R;Collet, C.; Joseph, R.; Nicholas, K.

Biochem. Biophys. Res. Commun. 164, 1380-1383, 1989
A;Title: Molecular cloning and characterization of a novel marsupial milk protein gene. A;Title: Molecular cloning and characterization of a novel marsupial milk protein gene. A;Reference number: A33672; MUID:90073674; PMID:2590207
A;Recession: A33672
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-176 <COL>
A;Residues: 1-176 <COL>
C;Superfamily: Lipocalin; Lipocalin homology
C;Superfamily: Lipocalin; Lipocalin homology
F;24-171/Domain: Lipocalin homology <LIP>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LGGGNLEATFTFMREDRCIOKKILMRKTEEPGKFSAYGGRKLIYLQELPGTDD---YVFY 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    late lactation protein A - tammar wallaby (fragments)
C;Species: Macropus eugenii (tammar wallaby)
C;bate: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 09-Jul-2004
C;Accession: A28561
R;Nicholas, K.R.; Messer, M.; Elliott, C.; Maher, F.; Shaw, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MKTLFLGVTLGLAAALS-----FTLEEEDITGTWYVKAMVVDKDFPEDRRPRKVSPVKV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 171; DB 2; Length 182; Pred. No. 6.7e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vomeronasal secretory protein I precursor - mouse N;Alternate names: probable pheromone carrier VNSP I C;Species: Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                       23.8%; Score 186.5; DB 2, 31.9%; Pred. No. 1.7e-11; ive 31; Mismatches 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
21.9%; Score 171; DB
Best Local Similarity 27.9%; Pred. No. 6.7e
Matches 38; Conservative 31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPROT:062471; EMBL:D38580
C;Superfamily: lipocalin; lipocalin homology
C;Keywords: carrier protein; glycoprotein
F;26-168/Domain: lipocalin homology <LIP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CVREFOGIQIREAELVGP 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CKDORRGGLRYMGKLVGP 131
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                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 31.94
Matches 44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57
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Cipate: 13, 5385-5842, 1994
A;Title: Possible pheromone-carrier function of two lipocalin proteins in the vomeronasa
A;Reference number: S51803
A;Reference acid sequence not shown
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-185 -MIY:
Cisage-references: Unipacelin; lipocalin homology
C;Superfamily: lipocalin; lipocalin homology
C;Keywords: carrier protein; glycoprotein
F;27-172/Domain: lipocalin homology <LIP>
                                    von Ebner's gland proteins 1 and
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A; Recession: $43648
A; Accession: $43648
A; Accession: $43648
A; Accession: $43648
A; Accession: $43648
A; Castus: preliminary
A; Molecule type: DNA
A; Residues: 1-177 «KOC>
A; Cross-references: GB:X74805; NID:9505300; PIDN:CAA52809.1; PID:9505301
C; Superfamily: lipocalin; lipocalin homology
F; 1-2.177/Product: hydrophobic molecule transporter VEG #status predicted «MAT>
F; 25-172/Domain: lipocalin homology «LP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 KTLEGGNLQVKFTVLIAGRCKEMSTVLEKTDEPAKYTAYSGKQVLYIIPSSVEDHYIFYY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55 TALGGGNLEATFTFMREDRCIQKKILMRKTEEPGKFSAYGGRKLIYLQELPGTDDYVFYC 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     late lactation protein precursor - tammar wallaby
C;Species: Macropus eugenii (tammar wallaby)
C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 09-Jul-2004
C;Accession: A33672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vomeronasal secretory protein II precursor - mouse
N;Alternate names: probable pheromone carrier VNSP II
C;Species: Mus musculus (house mouse)
C;Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C;Accession: S51803
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                                                                                                                                                                                                                                                                                                                                                               29.7%; Score 232; DB 2; 36.4%; Pred. No. 4.2e-16; tive 28; Mismatches 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26.2%; Score 205; DB 2;
33.3%; Pred. No. 2.4e-13;
iive 22; Mismatches 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               115 KDQRRGGLRYMGKLVGPCRCPHV 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 26.2%
Best Local Similarity 33.3%
Matches 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 36.4%
Matches 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21
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120 YDEYILMYTVKTKG 133
                  Query Match
Best Local Similarity 26.14
Matches 35; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Biformarinus (giant toad)
C;Date: 20-Feb-1995 #sequence revision 20-Feb-1995 #text_change 09-Jul-2004
C;Sate: 20-Feb-1995 #sequence revision 20-Feb-1995 #text_change 09-Jul-2004
C;Superimental source: choroid plaxus
A;Roserimental source: choroid plaxus
A;Roserimental source: choroid plaxus
A;Roserimental source: choroid from NCBI backbone (NCBIP:118239)
C;Superiment's lipocalin; lipocalin homology cLIP>
F;28-179/Domain: lipocalin homology cLIP>
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R;Engel, E.; Lepperdinger, G.; Richter, K.
submitted be EMBL Data Library, February 1995
A;Description: An mRNA expressed in the anterior-most part of the neural plate encodes a A;Reference number: $52354
A;Accession: $52354
A;Accession: $52354
A;Accession: $52354
A;Residue: preliminary
A;Molecule type: mRNA
A;Residues: 1-184 <ENGA
A;Cross-references: UNIPROT: Q91721; EMBL: X84414; NID: g666120; PIDN: CAA59132.1; PID: g6661
C;Superfamily: lipocalin; lipocalin homology
F;29-180/Domain: lipocalin homology <LIP>
                                         끍
Biochem. J. 241, 899-904, 1987
A;Title: A novel whey protein synthesized only in late lactation by the mammary gland
A;Reference number: A28561; MUID:87241271; PMID:3109381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 TVITPTADGNLDVVATFPKLDRCEKKSMTYIKTEQPGRFLSKSPRYGSDHVIRVVE-SNY 119
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C;Species: Xenopus laevis (African clawed frog)
C;Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MKTLFLGVTLGLAAALSF-----TLEEEDITGTWYVKAMVVDKD-FPEDRRPRKVSP
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                                                                                                                                                                                                                                       17.6%; Score 138; DB 2; Length 85; 40.4%; Pred. No. 6.7e-07; ive 15; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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6.3e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29.3%; Pred. ...
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                                                                                                             A;Molecule type: protein
A;Residues: 1-85 ANIC>
A;Cross-references: UNIPROT:P20462
C;Superfamily: lipocalin; lipocalin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 29.3%
Matches 36; Conservative
                                                                                                                                                                                                                                                              Best Local Similarity 40.49
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lipocalin - giant toad
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DEY 122
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A, Status: preliminary
A, Status: preliminary
A, Modecule type: protein
A, Modecule type: protein
A, Residues: 1-162 - KHAL>
A, Cross-references: UNIPROT: P33688
A, Cross-references: UNIPROT: P33688
A, Note: 162-Val was also found
R, Halliday, J.A.; Bell, K.; MoKenzie, H.A.; Shaw, D.C.
Comp. Biochem. Physiol. B 95, 773-779, 1990
A, Title: Feline whey proteins: identification, isolation and initial characterization of A, Reference number: A60525; MUID: 90263403; PMID: 2344734
A, Accession: E60525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   beta-lactoglobulin - eastern gray kangaroo
C;Species: Macropus giganteus (eastern gray kangaroo)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C;Accession: A29659
R;Godovac-Zimmermann, J.; Shaw, D.
Biol. Chem. Hoppe-Seyler 386, 879-886, 1987
A;Title: The primary structure, binding site and possible function of beta-lactoglobulin
A;Reference number: A29699; MUID:87299024; PMID:3620116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            beta-lactoglobulin III - cat

C;Species: Felis silvestris catus (domestic cat)

C;Species: Felis silvestris catus (domestic cat)

C;Date: 22-Nov-1993 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004

C;Accession: 833876; E60525

R;Halliday, J.A.; Bell, K.; McAndrew, K.; Shaw, D.C.

Protein Seq. Data Anal. 5, 201-205, 1993

A;Title: Feline beta-lactoglobulins I, II and III, and canine beta-lactoglobulins I and cat and dog.

A;Reference number: 833875
                                                                                                                                                                                                                                                                    51 PVKVTALGGGGGGAAATFTFMREDRCIQKKILMRKTEEPGKFSA----YGGRKLIYLQELPG 106
                                                                                                                                                                                                                                                                                                          20
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                                                                                                                                                                           1 MKTLFLGVTLGLAAAL, FT-----LEEEDITGTWYVKAMVVDKDFPEDRRPR-KVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 LEEEDITGTWYVKAM-----VVDKDFPEDRRPRKVSPVKVTALGGGNLEATFTFMREDR
                                                                        Gaps
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   Length 184;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |:||||| :||| | :| | | :| CVQKKILAQKTELPAEF-----KISYLDENELIVLDTDYENYLFFC 106
                                                                    Indels
15.4%; Score 120.5; DB 2; 26.1%; Pred. No. 9e-05; cive 26; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15.1%; Score 118; DB 2; 30.8%; Pred. No. 0.00014;
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F;10-160/Domain: lipocalin homology <LIP>
F;66-160,106-119/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20; Mismatches
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A;Molecule type: protein
A;Residues: 1-24 «HA2»
C;Superfamily: lipocalin; lipocalin homology
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A; Reference number: S33875
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A; Accession: S14507
A; Accession: S14507
A; Accession: S14507
A; Accession: S14507
A; Residues: 1-180 <-FOL.
A; Residues: 1-180 <-FOL.
A; Residues: 1-180 <-FOL.
A; Cross-references: EMBL:X58471; NID:g967; PIDN:CAA41385.1; PID:g968
B; Kim, J.
submitted to the EMBL Data Library, January 1993
A; Reference number: S42800
A; Accession: S42801
A; Molecule type: mRNA
A; Residues: 1-180 <-KIM>
A; Accession: S42801
A; Molecule type: mRNA
A; Residues: 1-32 <-KIZ
A; Accession: S42801
A; Molecule type: mRNA
A; Residues: 1-32 <-KIZ
A; Accession: S42801
A; Molecule type: mRNA
A; Residues: 1-32 <-KIZ
A; Cross-references: EMBL:Z19570; NID:g437753; PIDN:CAA79624.1; PID:g437754
C; Comment: Under physiological conditions beta-lactoglobulin exists as an equilibrium mic; Superfamily: signal sequence #status predicted <-KIG
C; Keywords: milk
C; Superfamily: signal sequence #status predicted <-KIG
F; 19-180/Pomain: signal sequence #status predicted <-KIG
F; 8-178/Domain: lipocalin homology <-LIP
F; 8-178/Domain: lipocalin homology <-LIP
F; 8-178/LPOmain: lipocalin homology <-LIP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51 PVKVTALGGGNLEATFTFMREDRCIQKKILMRKTEEPG--KFSAYGGRKLIYLQELPGTD 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13 EKFVGSWYLREAAKTMEFSIPLFDMDIKEVNLTP--EGNLELVL-LEKTDRCVEKKLLLK 69
                                                                                                                                                                                                        23 EDITGTWYVKAMVVDKDFPEDRRPRKVSPVKVTALGGGNLEATFTFMREDRCIQKKILMR 82
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                                                                                                         Length 155;
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13.7%; Score 107; DB 1; Length 180;
Best Local Similarity 28.5%; Pred. No. 0.0021;
Matches 37; Conservative 16; Mismatches 59; Indels
                                                                                                                                                         Indels
                                                                                                      DB 2;
                                                                                                                                                           44;
                                                                                                                                                                                                                                                                                                                    83 KTEEPGKFSAYGGRKLIYLQELPGT--DDYVFYC 114
                                                                                                                                                                                                                                                                                                                                                                      70 KTKKPTEFEIYISSESSYTFCVMETDYDSYFLFC 103
                                                                                                    Query Match
13.9%; Score 108.5; DB 2
Best Local Similarity 28.7%; Pred. No. 0.0012;
Matches 27; Conservative 18; Mismatches 44
A;Cross-references: UNIPROT:P11944
C;Superfamily: lipocalin; lipocalin homology
F;10-155/Domain: lipocalin homology <LIP>
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117 YKKYLLFCME 126
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beta-lactoglobulin I - dog

C;Species Canis lupus familiaris (dog)

C;Dete: 02-Dec-1993 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004

C;Accession: S33877; A61590

C;Accession: S33877; A61590

F;Halliday, J.A.; Bell, K.; McAndrew, K.; Shaw, D.C.

Protein Seq. Data Anal. 5, 201-205, 1993

A;Title: Feline beta-lactoglobulins I, II and III, and canine beta-lactoglobulins I and can and dog.
                                                                                                                                                                                                                                                                                                                                                                                                                                               R.Pervaiz, S.; Brew, K.
Arch. Biochem. Biophys. 246, 846-854, 1986
A.Title: Purification and characterization of the major whey proteins from the milks of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19 TLEBED---ITGTWYVKAMVVD--KDFPEDRRPRKVSPVKVTALGGGNLEATFTFMREDR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 CABQKVLAEKTEVPAEF-----KINYVEENQIFLLDTDYDNYLFFCE 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 161;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      le (Canis familiaris).
A;Reference number: A61590; MUID:86214061; PMID:3707136
A;Accession: A61590
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Pred. No. 0.0021;
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A,Residues: 'L',2-20,'A',22-26 <PER>
C,Superfamily: lipocalin; lipocalin homology
C,Superfamily: gland; min E,Fl0-159/Pomain: lipocalin homology <IP>
F;0-159/Pomain: lipocalin homology <IIP>
F;66-159,106-119/Disulfide bonds: #status predicted
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                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-161 -4ML>
A;Cross-references: UNIPROT: P33685
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28.7%;
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Best Local Similarity 28.79
Matches 31, Conservative
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June 7, 2005, 14:29:40 ; Search time 177 Seconds (without alignments) 422.393 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                         OM protein - protein search, using sw model
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US-10-049-372-4 782 1 MKTLFLGVTLGLAAALSFTL......KLVGPCRCPHVGSPGHLTCR 146 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 seqs, 512079187 residues Searched:

1612378 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

284.5 284.5 284.5 284.5 238.5 23	335.1 330.5 330.5 330.5	170 170 170 174 177 176 176 177		08PA HUMAN 08BB HUMAN 063613 VEGP HUMAN ALLI CANPA VEGP RAT VEGP PIG 086658 08K1H9	
679 28 623 28 623 28 623 274.5 274.5 238.5 2	886.8 336.4 31.2 30.6 30.5	170 176 176 176 177 177 176 176		OBPA_HUMAN OBPB_HUMAN 063613 VEGP_HUMAN ALLI_CANFA VEGP_PIG 086628 08K1H9 VEGT_RAT	
2 6 23 2 8 4 . 5 2 1 2 1 2 3 2 1 2 3 2 3 3 1 2 2 3 3 1 2 3 2 4 1 1 2 1 2 3 1 2 1 2 3 1 2 1 2 3 1 3 1 2 3 1 4 1 2 3 1 5 2 3 1 6 . 5 1 7 1 2 1 2 3 1 7 1 2 3 1 8 . 5 1 9 . 5 1 1 1 2 1 2 3 1 1 3 3 1 3 3 1 3 3 1 3 3 1 3 3	79.7 335.7 30.6 30.6 30.5	. 170 176 176 177 177 176 176		06BB HUMAN 063613 VEGP HUMAN ALLI CANFA VEGZ RAT VEGP PIG 086658 08KH99	
284.5 27	35.4 31.2 30.6 30.5 5.5	176 176 1774 176 176 176	0 0 0	Q63613 VEGP_HUMAN VEGZ_RAT VEGP_PIG Q86658 VEGI_RAT	
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238.5 238.5	30.5	176 176 176 177 174	488444	VEGP_PIG Q86638 Q8K1H9 VEG1_RAT	
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199.5 188.5 188.5 171 171 171 178.5	26.2		,	VNS2 MOUSE	_
188.5 186.5 163.1 103.1 123.5 123.5 123.5 121.5 121.5 119.5 117.5	25.5	176	4	LLP TRIVU	Q29144 trichosurus
186.5 171 171 171 178.5	24.1	176	~	Q71RT0	Q71rt0 macropus eu
171 178 178 178 178 178 178 178 178 178	23.8	176	-	LLPA_MACEU	P20462 macropus eu
163 128 123 123 123 121.5 121.5 2 120.5 119.5 119.5 117 6 117.5	21.9	182	Н	VNS1_MOUSE	_
80012640978	20.8	159		Q9JLX6	
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12.E4.2.2.C	15.6	183	-	LIPO_BUFMA	
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8 7	15.0	183	7	QBAWBB	
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180 163 163 181 189 189 191 191 180 186
1133 133 133 133 133 133 133 133 133 13
106.5 106.5 105.105 104.5 103 102 102 101 101 100
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ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 NLEATFTFMREDRCIQKKILMRKTEEPGKFSAYGGRKLIYLQELPGTDDYVFYCKDQRRG 120
                                                                                                                                                                                                                                                                                       GRNPWTNLEALEFKKLVQHKCLSBEDIFMPLGTGSCVLEH
-> ASAPCRAVPLSPRRLTWPPHLQVGILIPWRPWKNLRN
WCSTRDSRRRTFSCPCRREAAFSNTRQPPGLHLQSPPYHQT
QSPHLDLSSSHDFSLLPPT (in isoform Ag).
/FTId=vSP_003137.
F -> Y (in Ref. 1; CAB71326).
H -> R (in Ref. 1; CAB71326).
M -> T (in Ref. 1; CAB71326).
M -> T (in Ref. 1; CAB71326).
W, 391F555223629275 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                        By similarity.
ITGTWYVKAMVVDKDFPEDRRPRKVSPVKVTALGGGNLEAT
                                                                                                                                                   FTFMREDRCIOKKILMRKTEEPGKFSAYGGRKLIYLQELPG
DYDYYGYCORRGGIRMYMAKLU -> BGSSYHPERNEDAB
DGGAWQIORLWGQERHIPAGARDGRILRLLLLQRPAPMGPAL
HGKACGICSLQGRANVPILAHLATSPA (In isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MKTLFLGVTLGLAAALSFTLEBEDITGTWYVKAMVVDKDFPEDRRFRKVSPVKVTALGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NLEATFTFMREDRCIQKKILMRKTEEPGKFSAYGGRKLIYLQELPGTDDYVFYCKDQRRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SECUENCE FROM N.A. (ISOFORM BA).
MEDLINE-2887296; PubMed-12975309;
Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
Chen J., Chow B., Crowley C., Currell B., Deuel B., Dowd P.,
Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
                                                                                                                                                                                                                 Ad).
/FTId=VSP_003135.
RNPNTNLEALEEFKKLVQHKGLSEEDIFMPLQTGSCVLEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MKTLFLGVTLGLAAALSFTLEEEDITGTWYVKAMVVDKDFPEDRRPRKVSPVKVTALGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORMS BA; BB AND BG).
MEDLINE=20076326; PubMed=10607840; DOI=10.1093/hmg/9.2.289;
Lacazette B., Gachon A.-M., Pitiot G.;
A. novel human odorant-binding protein gene family resulting from genomic duplicons at 9q34: differential expression in the oral and genital spheres.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                        -> PCRCPHVGSPGHLTCR (in isoform Ab) /FTId=VSP_003136.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ob-JUL-2004 (Rel. 44, Last annotation update)
Odorant-binding protein 2b precursor (OBPIIb) (UNQ653/PRO1283)
Name=OBP2B;
InterPro; IPR011038; Calycin.
InterPro; IPR00266; Lipocln cytFABP.
InterPro; IPR002466; vonEbner_gland.
Pfam; PF00061; Lipocalin; I.
PROSITE; PS00213; LIPOCALIN; FALSE NEG.
Alternative splicing; Lipocalin; Olfaction; Signal; Transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                        Odorant-binding protein 2a.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 679; DB 1; 1
Pred. No. 1.3e-64;
                                                                                                                                                                                                                                                                                                                                                                                                                                  86.8%; Scor.
100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         170 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9NPH6; Q9NY51; Q9NY52;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation updat
                                                                                           Potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genital apheres.";
Hum. Mol. Genet. 9:289-301(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                 19318 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           130; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLRYMGKLVG 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 GLRYMGKLVG 130
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166
166
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149
159
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149 1
159 1
170 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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                                                                                                        CHAIN
DISULFID
VARSPLIC
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CONFLICT
CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                               VARSPLIC
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                                                                                           SIGNAL
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HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POCENTIAL.
Boxant-binding protein 2b.
By similarity.
YGGRKLMYLQELPRRDHYIFYCKDQHHGGLLHMGKLVGRNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DTNREALBEFKKLVQRKGLSEEDIFTPLQTGSCVPEH ->
CLSAVEMDQITPALWEALAIDTLRKLRIGTRRPRIRWGQEA
HVPAGAAQEGPLHLLLQRPAPWGPAPHGKACG (in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         isoform Bb).
/FTId=VSP_003138.
ITGTWYVKAMVVDKDFPEDRRPRKVSPVKVTALGGGKLEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FTFMREDRCIQKKILMRKTEEPGKYSAYGGRKLMYLQELPR
RDHYIFYCKDQHHGGLLHMGKLVGRNSDTNREALEEFKKLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QRKGLSEEDLFTPLQTGSCVPEH -> EGGSVHPEENPDAE
DGGAWQIQRLWGQBAHIPAGAAQEGPLHLLLQRPAPWGPAP
                                                                                                                                                                                   FUNCTION: Probably binds and transports small hydrophobic volatile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
Yi S., Yu G., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D.,
Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
Godowski P., Gray A.;
                                                                                                          "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: bioinformatics assessment."; denome Res. 13:2265-2270(2003).
                                                                                                                                                                                                                                                                                                                                                                  IsoId=Q9NPH6-3; Sequence=VSP_003139;
TISSUE SPECIFICITY: Strongly expressed in genital sphere organs
such as the prostate and mammary glands.
SIMILARITY: Belongs to the lipocalin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSÍTE; PSO0213; LIPOCALIN; FALSE NEG.
Alternative splicing; Lipocalin; Olfaction; Signal; Transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 170;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HGKACG (in isoform Bg).
/FTId=VSP 003139.
170 AA; 19456 MW; 344FBC37E70739C1 CRC64;
                                                                                                                                                                                                                                                         Event=Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 623; DB 1;
Pred. No. 1.3e-58;
4; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO; GO:0005549; F:odorant binding; NAS.
GO; GO:0007635; P:chemosensory behavior; TAS.
GO; GO:0007608; P:perception of smell; NAS.
InterPro; IPR011038; Calycin.
InterPro; IPR00566; Lipocln_cytFABP.
InterPro; IPR002450; vonEbner_gland.
PFGMG; Lipocalln; 1.
PROSITE; PS00213; LIPOCALIN; FALSE_NEG.
                                                                                                                                                                                                        molecules.
SUBCELLULAR LOCATION: Secreted (Probable)
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                IsoId=Q9NPH6-2; Sequence=VSP_003138;
                                                                                                                                                                                                                                                                           Name=Ba;
IsoId=Q9NPH6-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Potential
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, AJ251026; CAB71322.1;
EMBL, AJ251027; CAB71324.1;
EMBL, AJ251028; CAB71325.1;
EMBL, AX358991; AAQ89340.1;
Genew, HGNC:23381; OBP2B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AJ251025; CAB71322.1; -.
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91.5%;
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                                                                                                                                                                                                                                                                                                               Name=Bb;
                                                                                                                                                                                                                                                                                                                                                   Name=Bg;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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MKTLFLGVTLGLAAALSFTLEBEDITGTWYVKAMVVDKDFPEDRRPRKVSPVKVTALGGG

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NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                               rissue=Tears;
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                                                           61 KLEATFTFMREDRCIQKKILMRKTEEPGKYSAYGGRKLMYLQELPRRDHYIFYCKDQHHG 120
                                         NLEATFTFMREDRCIOKKILMRKTEEPGKFSAYGGRKLIYLQELPGTDDYVFYCKDQRRG 120
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    MKTLFLGVTLGLAAALSFTLEEEDITGTWYVKAMVVDKDFPEDRRPRKVSPVKVTALGGG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MKTLFLGV-TLGLAAALSFTL----EEEDITGTWYVKAMVVDKDFPEDRRPRKVSPVKVT
                                                                                                                                                                                                                                                                                                                                                                                                    .gattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUJ-1993 (Rel. 26, Created)
01-JUJ-1993 (Rel. 26, Last sequence update)
05-JUJ-2004 (Rel. 44, Last annotation update)
von Ebner's a gland protein precursor (VEG protein) (Tear prealbumin)
Name-LCN1, Synonyms-VEGP,
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-Fisher; TISSUB=Olfactory mucosa;
MEDLINE=9201476; Pubmed=1931961;
MedLINE=9201476; Pubmed=1931961;
Molecular Cloning of putative odorant-binding and odorant-metabolizing proteins.;
Biochemistry 30:10376-10382(1991).
BISHBL; M66734; AAA42307.1; -...
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                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36.4%; Score 284.5; DB 2; ilarity 44.4%; Pred. No. 3.1e-22; Conservative 21; Mismatches 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0005215; F:transporter activity; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IPR011038; Calycin.
InterPro; IPR000566; Lipocln.cytFABP.
InterPro; IPR002450; vonEbner_gland.
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                                                                                                                                                                                                                                                                176 AA
                                                                                                                                                                                                                                                                                                         Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VNEBNERGLAND.
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                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00061; Lipocalin; 1
PRINTS; PR01175; VNEBNERGLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                               Odorant-binding protein.
                                                                                                                         GLRYMGKLVG 130
                                                                                                                                                  121 GLLHMGKLVG 130
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Matches 60; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60;
                                                                                                                                                                                                                                                                                                                                                                                       Name=RY2G12;
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                                               61
                                                                                                                             121
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                                                                                                                                                                                                                                                                                    063613;
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Q63613
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the gene encoding the human lipocalin tear the recombinant protein in Escherichia
                                                                                   Blacker M., Kock K., Ahlers C., Buck F., Schmale H.; a member of the "Molecular cloning of human von Ebner's gland protein, a member of the lipocalin superfamily highly expressed in lingual salivary glands."; Biochim. Biophys. Acta 1172:131-137(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              necessary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=94156196; PubMed=8112601; DOI=10.1016/0378-1119(94)90752-8;
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                                                                                                                                                                                                                                                                                                                MEDLINE=93015903; PubMed=1400345; Redl B., Holzfeind P., Lottspeich F.; "cDNA cloning and sequencing reveals human tear prealbumin to b member of the lipophlilc-ligand carrier protein superfamily."; J. Biol. Chem. 267:20282-20287(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=93272888; PubMed=8500570; DOI=10.1006/exer.1993.1075; Lassagne H., Gachon A.-M.; "Cloning of a human lacrimal lipocalin secreted in tears."; Exp. Eye Res. 56:605-609(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Expression of a lipocalin in human nasal mucosa."; Comp. Biochem. Physiol. 1188:819-824(1997).
-i- FUNCTION: Could play a role in taste reception. Could be for the concentration and delivery of sapid molecules in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Nasal mucus;
Scalfari F., Castagna M., Fattori B., Andreini I., Maremmani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00061; Lipocalin; 1.
PROSITE; PS00213; LIPOCALIN; FALSE NEG.
Direct protein sequencing; Lipocalin; Signal; Transport.
SIGNAL
                                        IISSUE=Tongue;
MEDLINE=93176795; PubMed=7679926;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, X62418, CAA4284.1;
EMBL, X67647; CAA47889.1;
EMBL, L14927; AAA18633.1;
EMBL, M90424; AAA61845.1;
PIR; A44029; LCHUL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Structural organization of prealbumin and synthesis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genew; HGNC:6525; LCN1.
MIM; 151675; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene 139:177-183(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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SEQUENCE OF 19-38.
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                                                       PVKVTALGGGNLEATFTFMREDRCIQKKILMRKTEEPGKFSAYGGRKLIYLQELPGTDDY 110
                                                                          FUNCTION: Could play a role in taste reception. Could be necessary for the concentration and delivery of sapid molecules in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MKTLFLGVTLGLAAALS----FTLEEEDITGTWYVKAMVVDKDFPEDR-RPRKVSPVKV
                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
STRAIN-WHISTART; STSSUB-Lingual sallvary gland;
MEDLINE-94237155; Pubmed-75.4123;
Kock K., Ahlers C., Schmale H.;
Structural organization of the genes for rat von Ebner's gland
proteins 1 and 2 reveals their close relationship to lipocalins.";
Eur. J. Biochem. 221:905-916 (1994).
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8
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PROSITE; PS00213; LIPOCALIN; FALSE NEG.
Direct protein sequencing; Lipocalin; Multigene family; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30.6%; Score 239; DB 1; Length 177; 37.1%; Pred. No. 2.4e-17; tive 28; Mismatches 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Von Ebner's gland protein
                                                                                                                                                                                                                                                                                     01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Von Ebner's gland protein 2 precursor (VEG protein 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73149ABD1F52EC15 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             qustatory system.
-!- SUBUNIT: Homodimer (By similarity).
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the lipocalin family.
                                                                                                                                                                                                                                                      177 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               By similarity
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IPR002450; vonEbner_gland.
                                                                                                                          111 VFYCKDQRRGGLRYMGKLVG 130
                                                                                                                                                  : ||: : | ||: |
115 ILYCEGELHGRQIRMAKLLG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                177 AA; 19699 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, X74806; CAA52810.1; -.
EMBL, X74807; CAA52811.1; -.
PIR, S43647; S43647.
INCERPO, IPRO11038; Calycin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53; Conservative
                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
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                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxiD=10116;
                                                                                                                                                                                                                                                                                                      01-FEB-1995
05-JUL-2004
                                                                                                                                                                                                                                                                                                                                                             Name=Vegp2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transport.
                                                       21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                     60 TILEGGNLEAKVTMLISGRCOEVKAVLEKTDEPGKYTADGGKHVAYIIRSHVKDHYIFYC 119
                                                                                                                                                                             1 MKPLLLAVSLGLIAALQAHHLLASDEEIQDVSGTWYLKAMTVDREFPE-MNLESVTPMTL 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=98158930; PubMed=9497502;
Konieczny A., Morgenstern J.P., Bizinkauskas C.B., Lilley C.H.,
Brauer A.W., Bond J.F., Aalberse R.C., Wallner B.P., Kasaian M.T.;
"The major dog allerges Can f 1 and Can f 2, are sallvary lipocalin proteins: cloning and immunological characterization of the
                                                                                                                                            1 MKTLFLGVTLGLAAALS----FTLEEE--DITGTWYVKAMVVDKDFPEDRRPRKVSPVKV
                                                                                                                                                                                                                  55 TALGGGNLEATFIFMREDRCIQKKILMRKTEEPGKFSAYGGRKLIYLQELPGTDDYVFYC
                                                                                                           Gaps
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Canis.
                                                                                                           11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16;
                                                                        DB 1; Length 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 174;
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                                                                                                           Indels
   Von Ebner's gland protein.
                    By similarity.
ODDBF124C8C78CB8 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Edulb idmiliaile (Voy.)
Eukaryola: Merezoa: Choydata; Craniata; Vertebrata;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunology 92:577-586 (1997).
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Tongue epithelial tissue.
-!- Acauses an allergic reaction in human.
-!- SIMILARITY: Belongs to the lipocalin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2003 (Rel. 42, Last annotation update)
Major allergen Can f 1 precursor (Allergen Dog 1).
Canis familiaris (Dog).
                                                                    Match 35.1%; Score 274.5; DB 1; Local Similarity 42.3%; Pred. No. 3.7e-21; les 58; Conservative 27; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31.2%; Score 244; DB 1; 35.7%; Pred. No. 6.9e-18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29; Mismatches
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N-linked (Glc)
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InterPro; IPR000566; Lipocln_cytFABP.
InterPro; IPR0002450; vonEbner_gland.
PR0001; Lipocalin; IPR00119; PROSITE; PS00213; LIPOCALIN; FALSE_NEG.
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19 176 Vc
79 171 B;
176 AA; 19250 MW;
                                                                                                                                                                                                                                                                                                           :: | | :: |: 120 EGELHGKPVRGVKLVGR 136
                                                                                                                                                                                                                                                                                       115 KDQRRG----GLRYMGK 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19248 MW;
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Best Local Similarity 35.74
Matches 50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                 CANFA
                  DISULFID
SEQUENCE
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                                                                        Query Match
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018873;
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                                                                                                         Matches
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54

1 MKTLFLGVTLGLAAALSFTLEEED-----ITGTWYVKAMVVDKDFPEDRRPRKVS

Gaps

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53 KVTALGGGNLEATFTFMREDRCIQKKILMRKTEEPGKFSAYGGRKLIYLQELPGTDDYVF 112
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                                                         ; || ||:||| ||: :| ::::|| :| |:|| |:::|| 59 ILKALEGGDLEAQITFLIDGQCQDVTLVLKKTNQPFTFTAYDGKRVVYILPSKVKDHYIL 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDITINE=22939397; PubMed=14578123; Guiraudie G., Pageat P., Cain A.H., Madec I., Meillour P.N.; Guiraudie G., Pageat P., Cain A.H., Madec I., Meillour P.N.; Functional characterization of olfactory binding proteins for appearing compounds and molecular cloning in the vomeronasal organ of pre-pubertal pigs."; Chem. Senses 28:609-619(2003).

EMBL; AX177149; AAO18367.1; -.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           176 AA; 19368 MW; AF7C2D750D4AC4AB CRC64;
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
25-0CT-2004 (TrEMBLrel. 28, Last annotation update)
CDNA sequence BC027556 (Lipocalin 13)
Name=BC027556; Synonyms=Lcn13;
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. 24, Created)
(TrEMBLrel. 24, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P02754; 1QG5.
GO; GO:0005215; F:transporter activity; IEA.
GO; GO:0006810; P:transport; IEA.
                                                                                                                                                                                                                                                                                                                                                                                      176 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR011038; Calycin.
InterPro; IPR000566; Lipocln_cytEABP.
InterPro; IPR002456; vonBbner_gland.
Pfam; PF00061; Lipocalin; 1.
PRINTS; PR01175; VNEBNERGLAND.
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                                                                                                                                                         113 YCKDORRGGLRYMGKLVG 130
                                                                                                                                                                                                                      119 YCEGELDGOEVRMAKLVG 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30.5%;
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Matches 50; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Von Ebner gland protein.
Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2003
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q8K1H9
                                                                                                                                                                                                                                                                                                                                                                                          986688
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61 KTLEGGNLQVKFTVLISGRCQEMSTVLEKTDEPGKYTAYSGKQVVYSIPSAVEDHYIFYY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene 202:61-67(1997).

-!- FUNCTION: Could play a role in taste reception. Could be necessary for the concentration and delivery of sapid molecules in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-96087418; PubMed-9427546; DOI=10.1016/S0378-1119(97)00454-X; Holzfeind P., Merschak P., Wojnar P., Redl B.; Structure and organization of the porcine LCN1 gene encoding Tear lipocalin/von Ebner's gland protein.";
                                                                                                                                                                                                                                                                                                                                P537<u>T</u>5; 019136;
01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Von Ebner's gland protein precursor (VEG protein) (Tear prealbumin)
(TE) (Tear lipocalin) (Lipocalin-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Suina, Suidae, Sus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30.5%; Score 238.5; DB 1; Length 176; 36.2%; Pred. No. 2.7e-17; tive 30; Mismatches 47; Indels 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Von Ebner's gland protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            By similarity.
G -> A (in Ref. 2).
BB7D6D750D4AC4AB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE=9531641; PubMed=7796060;
Garibotti M., Christansen H., Schmale H., Pelosi P.;
"Porcine VEG proteins and tear prealbumins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gustatory system.
-!- SUBUNIT: Homodimer.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the lipocalin family.
                                                                                                                                                                                                                                                                                              176 AA
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InterPro; IPR011038; Calycin.
InterPro; IPR000566; Lipocln_cytFABP.
InterPro; IPR002450; vonBoner_gland.
                                                                    115 KDQRRGGLRYMGKLVGPCRCPHV 137
                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19352 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chem. Senses 20:69-76(1995).
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                                                                                                                                                                                                                                                                                                 STANDARD;
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136 1
176 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=LCN1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S:
Matches 50
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                                                                                                                                                                                                                                           RESULT 7
                                                                                                                                                                                                                                                                                                        បភុឌ្ឍនាធានស្តេក្សនាន្ទីនុងស្ម័ន្ទនាន់នុងស្ថិក្សន្តិក្សាស្ត្រស្តិក្សាស្ត្រស្តិក្សាស្ត្រស្តិក្សាស្ត្រស្តិក្សាស្
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Query Match
Best Local S
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                                   A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Straubberg R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Stachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

By Hopking R.F., Jordan H., More T., Max S.I., Wang J., Hsieh F.,

A papleton M., Soares M.B., Bonaldo M.F., Casavant T.D., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Tocahiyuki S., Carninci P., Prange C.,

Brownstein M.J., Usdin T.B., Tocahiyuki S., Carninci P., Prange C.,

Brownstein M.J., Usdin T.B., Tocahiyuki S., Carninci P., Prange C.,

Brownstein M.J., Wokin T.B., Tocahiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brokask S.A., McKennan K.J., Madek J.A., Gunzane P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rachy J., Helton B., Ketteman M., Madan A., Young A., Sodergren E.J., Lu X., Gibbs R.A.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

K. Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

T. "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54 VTALGGGNLEATFTFMREDRCIQKKILMRKTEEPGKFSAYGGRKLIYLQELPGTDDYVFY 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MKTLFLGV-TLGLAAALSFTLEEE-----DITGTWYVKAMVVDKDFPEDRRPRKVSPVK 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MKSLILITILLIGIVAVIK--AQEAPPDDLVDYSGIWYAKAMVHNGTLPSHKIPSIVFPVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Suzuki K., Lareyre J.J., Sanchez D., Gutierrez G., Araki Y., Matuaik R.J., Orgebin-Crist M.C.; "Molecular evolution of epididymal lipocalin genes localized on mouse chromosome 2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10;
                        MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 176;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     176 AA; 19996 MW; 1AE75207D6C70B2F CRC64;
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01-FEB-1991 (Rel. 17, Last sequence update)
05-ULL-2004 (Rel. 44, Last amotation update)
Von Ebner's gland protein 1 precursor (VEG protein 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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38.4%; Pred. No. 5.1e-17;
iive 26; Mismatches 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GEGE 339:49-59(2004).

EMBL, BC027556, AAH27556.1; -.

EMBL, AX360148, AAR1375.1; -.

MGD, MGI:2387617, BC027556.

GO, GO:0005215; F:transporter activity, IEA.

GO, GO:0006810; P:transport; IEA.
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InterPro; IPR000566; Lipocln_cytFABP.
InterPro; IPR002450; vonEbner_gland.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=B6D2F1; TISSUE=Epididymis;
PubMed=15363845;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119 CEGRHNGTSSFGMGKLMG 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR01175; UNEBNERGLAND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00061; Lipocalin; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and mouse cDNA sequences."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Uterus;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55 TALGGGNLEATFTFWREDRCIOKKILMRKTEEPGKFSAYGGRKLIYLQELPGTDDYVFYC 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 KTLEGGNLQVKFTVLIAGRCKEMSTVLEKTDEPAKYTAYSGKQVLYIIPSSVEDHYIFYY 120
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                                                                                                                                                                                                                                STRAIN=Wister; TISSUB=Lingual salivary gland; MEDLINE=90136923; PubMed=1689010; DOI=10.1038/343366a0; Schmale H., Holtgreve-Grez H., Christiansen H.; Possible role for salivary gland protein in taste reception indicated by homology to lipophilic-ligand carrier proteins."; Nature 343:366-369(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=94237155; PubMed=7514123; MEDLINE=94237155; PubMed=7514123; MEDLINE=94237155; PubMed=7514123; MEDLINE=94237155; PubMed=7514123; MCoK K., Ahlers C., Schmale H.; Structural organization of the genes for rat von Ebner's gland proteins 1 and 2 reveals their close relationship to lipocalins."; Eur. J. Biochem. 221:965-916(1994).

-!- FUNCTION: Could play a role in taste reception. Could be necessary for the concentration and delivery of sapid molecules in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MKTLFLGVTLGLAAALS----FTLEEEDITGTWYVKAMVVDKDFPEDR-RPRKVSPVKV
Name=Vegpl; Synonyms=Vegp;
Rattus norvegicus (Rat).
Ebkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Libocalin; Multigene family; Signal; Transport.
SIGNAL
SIGNAL
1 18 Potential.
17 Von Bbner's gland protein 1.
DISULPID 80 172 By similarity.
SEQUENCE 177 AA; 19725 MW; CCA36A7F544D6707 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gustatory system.
-!- SUBUNIT: Homodimer (By similarity).
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the lipocalin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         174 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, X52016; CAA36263.1; -.
EMBL, X74805; CAA52809.1; -.
PIR; S08161; S08161.
InterPro; IPR011038; Calycin.
InterPro; IPR001656; Lipocln_cytFABP.
InterPro; IPR002450; vonEbner_gland.
Ffan; PF00061; Lipocalin; 1.
PROSITE; PS00213; LIPOCALIN; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 115 KDQRRGGLRYMGKLVGPCRCPHV 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 EGKIHRHHFQIAKLVG--RDPEI 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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36.48; F.
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Q8SQ30;
28-FEB-2003 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52; Conservative
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                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                     NCBI_TaxID=10116;
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NCBI_TaxID=10090;
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    ID DIT AND SERVICE SER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 SNGDLEAKFTTNANGICEEIKMKFEKTDKPGIFSTNDGSRQVLIEKTSVRDHWILFCEGE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57
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                                                                                                                                                                                                                      TISSUE-Mammary gland;
MEDLINE=21856506; PubMed=11867236; DOI=10.1016/S0378-1119(01)00883-6;
Trott J.F., Wilson M.J., Hovey R.C., Shaw D.C., Nicholas K.R.;
"Expression of novel lipocalin-like milk protein gene is developmentally-regulated during lactation in the tammar wallaby, Gene 283:287-297(2002).
                                                                                                                                                                                                                                                                                                                                                                              -i- FUNCTION: Probably serves a role in the transport of a small ligand released during the hydrolysis of milk fat.
--- SUBCELLUAR LOCATION: Secreted.
--- TISSUE SPECIFICITY: Mammary gland specific. Secreted in milk.
--- DEVELOPMENTAL STAGE: Produced during the late phase of lactation.
--- SIMILARITY: Belongs to the lipocalin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q62472;
15-UUL-1998 (Rel. 36, Created)
15-UUL-1998 (Rel. 36, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Vesomeral secretory protein II precursor (VNSP II) (Lipocalin 4).
                                                                                                             Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Metatheria, Diprotodontia, Macropodidae, Macropus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61C48B673226EDA4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Late lactation protein B. By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27.9%; Score 218.5; DB 1
35.1%; Pred. No. 3.8e-15;
iive 28; Mismatches 56
  28-FEB-2003 (Rel. 41, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update) Late lactation protein B precursor (LLP-B).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, ARSIANO, CALONIO, INTERPROPERTO, IPRO1018; Calycin. InterPro; IPR000566; Lipocin.cytFABP. InterPro; IPR002450; vonEbner_gland.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                             Macropus eugenii (Tammar wallaby)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF319463; AAL85634.1; -.
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121 LHGMQVRIAKLLGP 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          174 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                 NCBI_TaxID=9315;
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                                                                        Name=LLPB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    into
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                                              Miyawaki A., Matsushita F., Ryo Y., Mikoshiba K.;
"Possible pheromone-carrier function of two lipocalin proteins in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                    FUNCTION: Transport of lipophilic molecules, possible pheromone-
                                                                                                                                                                                                                                                                                                                                                                            -!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Specifically expressed in vomeronasal and posterior glands of the nasal septum, the ducts of which open the lumen of the vomeronasal organ.
-!- SIMILARITY: Belongs to the lipocalin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Metatheria, Diprotodontia, Phalangeridae, Trichosurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22;
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SignAL 1 19 Potential.
CHAIN 20 185 Vesomeral secretory protein II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 205; DB 1; Length 185;
Pred. No. 1.1e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52; Indels
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D93702D4FA5344AB CRC64;
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MEDLINE=98154412; PubMed=9493361;
Piotte C.P., Hunter A.K., Marshall C.J., Grigor M.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
30-WAY-2000 (Rel. 39, Last annotation update)
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33.3%; Pred. No. 1...
22; Mismatches
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Trichosurus vulpecula (Brush-tailed possum)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00061; Lipocalin; 1.
PROSITE; PS00213; LIPOCALIN; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR, S51803; S51803.
MGD; MGI:102668; Lcn4.
InterPro; IPR011038; Calycin.
InterPro; IPR000566; Lipocin cytFABP.
InterPro; IPR002450; vonEbner_gland.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            107 TDDYVFYCKDQRRGGLRYMGKLVG 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | |: ||: | |: | |: | |: | |:| | |:| | |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| 
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MEDLINE=95112792; PubMed=7813422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      185 AA; 21399 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; D38581; BAA07582.1; -.
                                                                                                                                                                       vomeronasal organ.";
EMBO J. 13:5835-5842(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48; Conservative
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                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53 KVTALGGGNLEATFTFMREDRCIQKKILMRKTEEPGKFSAYGGRKLIYLQELPGTD---D 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57 TIMYLDDGKWEARFTWKKDDNCEEINIMLEKTADPRKITM--NRRLRYTCAAVRTSKQKH 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Phylogenetic analysis of three lipocalin-like proteins present in the milk of Trichosurus vulpecula (Phalangeridae, Marsupialia).";
J. Mol. Evol. 46:361-369(1998).
I. Hol. Evol. 46:361-369(1998).
I. FUNCTION: Probably serves a role in the transport of a small ligand released during the hydrolysis of milk fat.
I. SUBCELMULAR LOCATION: Secreted.
IISSUE SPECIFICITY: Mammary gland. Secreted in milk.
IISSUE SPECIFICITY: Mammary gland. Secreted in milk.
IISSUE SPECIPICITY: Holongs to the lipocalin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MKTLFLGVTLGLAAAL-----SFTLEEEDITGTWYVKAMVVDKDFPEDRRPRKVSPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25.5%; Score 199.5; DB 1; Length 176;
34.5%; Pred. No. 4.2e-13;
.ive 24; Mismatches 52; Indels 17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Metatheria, Diprotodontia, Macropodidae, Macropus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Trock J.F., Adams T.E., Wilson M., Nicholas K.R.,
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF348406, AAQ1517.1;
GO, GO:000515; F:transporter activity, IEA.
GO, GO:0006810; P:transport; IEA.
InterPro; IPR001039; Callycin.
InterPro; IPR00566, Lipocln. CytFABP.
InterPro; IPR00566, Lipocln. CytFABP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Late lactation protein.
By similarity.
325138B2468F017D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      176 AA; 20638 MW; 399D8D8EDE1F1C8A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              176 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR011038; Calycin.
InterPro; IPR000566; Lipocln cytFABP.
InterPro; IPR002450; vonEbner_gland.
Pfam; PF00061; Lipocalni, 1.
PROSITE; PS00213; LIPOCALIN; FALSE NEG.
Lipocalin; Milk; Signal; Transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              110 YVFYCKDQRRGGLRYMGKLVGP 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   176 AA; 20598 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL: U34287; AAA93179.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; Prodoci, Libocalin; 1. PRINTS; PRO1175; VNEBNERCLAN SEQUENCE 176 AA; 20638 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Late lactation protein-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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Q71RT0
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                                                                                                                                                                                                     57 LGGGNLEATFTFMREDRCIQKKILMRKTEEPGKFSAYGGRKLIYLQELPGTDD---YVFY 113
                                                                                                                                                                                                                                  61 LNNGKØRAKFTVKKDNNCEEINLTLEKIDEPRKITT--NRHLHHICDTVRTSEEKYWILS 118
                                                                                                     26
                                                                                                                                                    9
                                                                                                                               1 MKTLFLGVTLGLAAAL---SFTLEE-EDITGTWYVKAMVVDKDFPEDRRPRKVSPVKVTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |5]
SIMILARITY TO THE LIPOCALIN FAMILY.
MEDLINE=93222225; PubMed=8466952; DOI=10.1016/0005-2760(93)90165-6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Collet C., Joseph R.; "A novel member of the lipocalin superfamily: tammar wallaby late-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=90073674; PubMed=2590207;
Collet C., Joseph R., Nicholas K.R.;
"Molecular cloning and characterization of a novel marsupial milk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Metaheria; Diprotodontia; Macropodidae; Macropus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 19-87 AND 116-131.
MEDLINE=87241271; PubMed=3109381;
Nicholas K.R., Messer M., Elliot C., Maher F., Shaw D.C.;
"A novel whey protein synthesized only in late lactation by the mammary gland from the tammar (Macropus eugenii).";
                                                 6
     Length 176;
                                                 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biochem. Biophys. Res. Commun. 164:1380-1383 (1989)
     DB 2;
; Score 188.5; DB 2
; Pred. No. 6.4e-12;
31; Mismatches 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1991 (Rel. 17, Created)
01-FRB-1991 (Rel. 17, Last sequence update)
02-ULJ-2004 (Rel. 44, Last annotation update)
Late lactation protein A precursor (LLP-A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  176 AA
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PIR; A28561; A28561.
PIR; A3672; A33672.
InterPro; IPR011038; Calycin.
InterPro; IPR000566; Libocln_cytFABP.
InterPro; IPR002450; vonEbner_gland.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Macropus eugenii (Tammar wallaby)
                                                                                                                                                                                                                                                                                                           114 CKDQRRGGLRYMGKLVGP 131
                                                                                                                                                                                                                                                                                                                                                       CVREFQGKQIREAELVGP 136
     24.1%;
                                                      44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=LLPA;
     Query Match
Best Local 3
                                                                                                                                                                                                                                                                                                                                                          119
                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 15
LLPA_MACEU
                                                      Matches
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4
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                                                                                                                                                                                                                                                                                                          1 MKTLFLGVTLGLAAAL---SFTLEE-EDITGTWYVKAMVVDKDFPEDRRPRKVSPVKVTA 56
                                                                                                                                                                                                                                           9; Gaps
PFGM, PF00061; Lipocalin; 1.

PROSITE; PS00213; LIPOCALIN; FALSE NEG.

Direct protein sequencing; Lipocalīn; Milk; Signal; Transport.

SIGNAL

CHAIN

DISULFID

78 171 By similarity.

CONFLICT

59 59 T -> S (in Ref. 2).

CONFLICT

SEQUENCE 176 AA; 20612 MW; B327EA4F09DED435 CRC64;
                                                                                                                                                          Query Match 23.8%; Score 186.5; DB 1; Length 176; Best Local Similarity 31.9%; Pred. No. 1e-11; Matches 44; Conservative 31; Mismatches 54; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: June 7, 2005, 14:39:31
Job time : 181 secs
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119 CVREFQGTQIREAELVGP 136
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